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 Gerritsen, Mary E.
 Goddard, Audrey
 Godowski, Paul J.
 Grimaldi, J. Christopher
 Gurney, Austin L.
 Hillan, Kenneth J
 Kljavin, Ivar J.
 Kuo, Sophia S.
 Napier, Mary A.
 Pan, James;
 Paoni, Nicholas F.
 Roy, Margaret Ann
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 Wood, William I.
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Phe	Leu	Val	Pro	Leu	Gly	Ile	Thr	Asn	Ile	Ala	Ile	Asp	Phe	Gly
				20					25					30

Glu	Gln	Ala	Leu	Asn	Arg	Gly	Ile	Ala	Ala	Val	Lys	Glu	Asp	Ala
				35				40						45

Val	Glu	Met	Leu	Ala	Ser	Tyr	Gly	Leu	Ala	Tyr	Ser	Leu	Met	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

				50						55					60
Phe	Phe	Thr	Gly	Pro	Met	Ser	Asp	Phe	Lys	Asn	Val	Gly	Leu	Val	
				65					70					75	
Phe	Val	Asn	Ser	Lys	Arg	Asp	Arg	Thr	Lys	Ala	Val	Leu	Cys	Met	
				80					85					90	
Val	Val	Ala	Gly	Ala	Ile	Ala	Ala	Val	Phe	His	Thr	Leu	Ile	Ala	
				95					100					105	
Tyr	Ser	Asp	Leu	Gly	Tyr	Tyr	Ile	Ile	Asn	Lys	Leu	His	His	Val	
				110					115					120	
Asp	Glu	Ser	Val	Gly	Ser	Lys	Thr	Arg	Arg	Ala	Phe	Leu	Tyr	Leu	
				125					130					135	
Ala	Ala	Phe	Pro	Phe	Met	Asp	Ala	Met	Ala	Trp	Thr	His	Ala	Gly	
				140					145					150	
Ile	Leu	Leu	Lys	His	Lys	Tyr	Ser	Phe	Leu	Val	Gly	Cys	Ala	Ser	
				155					160					165	
Ile	Ser	Asp	Val	Ile	Ala	Gln	Val	Val	Phe	Val	Ala	Ile	Leu	Leu	
				170					175					180	
His	Ser	His	Leu	Glu	Cys	Arg	Glu	Pro	Leu	Leu	Ile	Pro	Ile	Leu	
				185					190					195	
Ser	Leu	Tyr	Met	Gly	Ala	Leu	Val	Arg	Cys	Thr	Thr	Leu	Cys	Leu	
				200					205					210	
Gly	Tyr	Tyr	Lys	Asn	Ile	His	Asp	Ile	Ile	Pro	Asp	Arg	Ser	Gly	
				215					220					225	
Pro	Glu	Leu	Gly	Gly	Asp	Ala	Thr	Ile	Arg	Lys	Met	Leu	Ser	Phe	
				230					235					240	
Trp	Trp	Pro	Leu	Ala	Leu	Ile	Leu	Ala	Thr	Gln	Arg	Ile	Ser	Arg	
				245					250					255	
Pro	Ile	Val	Asn	Leu	Phe	Val	Ser	Arg	Asp	Leu	Gly	Gly	Ser	Ser	
				260					265					270	
Ala	Ala	Thr	Glu	Ala	Val	Ala	Ile	Leu	Thr	Ala	Thr	Tyr	Pro	Val	
				275					280					285	
Gly	His	Met	Pro	Tyr	Gly	Trp	Leu	Thr	Glu	Ile	Arg	Ala	Val	Tyr	
				290					295					300	
Pro	Ala	Phe	Asp	Lys	Asn	Asn	Pro	Ser	Asn	Lys	Leu	Val	Ser	Thr	
				305					310					315	
Ser	Asn	Thr	Val	Thr	Ala	Ala	His	Ile	Lys	Lys	Phe	Thr	Phe	Val	
				320					325					330	
Cys	Met	Ala	Leu	Ser	Leu	Thr	Leu	Cys	Phe	Val	Met	Phe	Trp	Thr	
				335					340					345	

Pro	Asn	Val	Ser	Glu	Lys	Ile	Leu	Ile	Asp	Ile	Ile	Gly	Val	Asp
				350					355					360
Phe	Ala	Phe	Ala	Glu	Leu	Cys	Val	Val	Pro	Leu	Arg	Ile	Phe	Ser
				365					370					375
Phe	Phe	Pro	Val	Pro	Val	Thr	Val	Arg	Ala	His	Leu	Thr	Gly	Trp
				380					385					390
Leu	Met	Thr	Leu	Lys	Lys	Thr	Phe	Val	Leu	Ala	Pro	Ser	Ser	Val
				395					400					405
Leu	Arg	Ile	Ile	Val	Leu	Ile	Ala	Ser	Leu	Val	Val	Leu	Pro	Tyr
				410					415					420
Leu	Gly	Val	His	Gly	Ala	Thr	Leu	Gly	Val	Gly	Ser	Leu	Leu	Ala
				425					430					435
Gly	Phe	Val	Gly	Glu	Ser	Thr	Met	Val	Ala	Ile	Ala	Ala	Cys	Tyr
				440					445					450
Val	Tyr	Arg	Lys	Gln	Lys	Lys	Lys	Met	Glu	Asn	Glu	Ser	Ala	Thr
				455					460					465
Glu	Gly	Glu	Asp	Ser	Ala	Met	Thr	Asp	Met	Pro	Pro	Thr	Glu	Glu
				470					475					480
Val	Thr	Asp	Ile	Val	Glu	Met	Arg	Glu	Glu	Asn	Glu			
				485					490					

<210> 8
 <211> 535
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 33, 66, 96, 387
 <223> unknown base

<400> 8
 cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50
 tgagcttctg gtgcnttttg gctctaattc tggccacaca gagaancagt 100
 cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
 agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200
 tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250
 aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300
 ggccacatc aagaagttca ccttcgtctg catggctctg tcaactcacgc 350
 tctgtttcgt gatgttttgg acaccaacg tgtctngaa aatcttgata 400
 gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450

gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcattctca 500

ccgggtgggt gatgacactg aagaaaacct tcgtc 535

<210> 9

<211> 434

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361

<223> unknown base

<400> 9

tgacggaatc ccgggctggg tatcctggtt tngacaagat aaacccccag 50

caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100

agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150

gttttggaca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200

tggantttgc ctttgcagaa ntttgnngtg ttcctttgcg gattttctcc 250

tttttcccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350

ttgtcctnat ngccagcctt gtggctctac cctacctggg ggtgcacggt 400

gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10

<211> 154

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 33, 49, 68, 83, 90, 98, 119

<223> unknown base

<400> 10

tattcccagt tccggtcacg gggagggcgc atntcaccgg gtggctgang 50

acactgaaga aaaccttngt ccttgccccc agntttgtgn tgcggatnat 100

cgtcctcatc gccagcctng tggctctacc ctacctgggg gtgcacggtg 150

agac 154

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt tcttgggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gctctgtcac tcacgctc 18

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcatctcttc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttccgcca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
gcctgctgtg gtcacaggtc tccg 24

<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 18
gccccgcgcc cggcgccggg cgcccgaagc cgggagccac cgccatgggg 50
gcctgcctgg gagcctgctc cctgctcagc tgcgcgtcct gcctctgcgg 100
ctctgcccc tgcatcctgt gcagctgctg ccccgccagc cgcaactcca 150
ccgtgagccg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg 200
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250
ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300
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gccacggcgg ccttcttctt cttctttttc accctgctca tgctctgcgt 400
gagcagcagc cgggaccccc gggtgccat ccagaatggg ttttggttct 450
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gacggctcct tcaccaacat ctggttctac ttcggcgtcg tgggctcctt 550
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tacgcaggcc tcttcttctt cactctcctc ttctacttgc tgtcgatcgc 700
ggccgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750
agggcaaggt cttcatcagc ctcaacctca ccttctgtgt ctgcgtgtcc 800
atcgctgctg tcctgcccac ggtccaggac gccagccca actcgggtct 850
gctgcaggcc tcggctcatca ccctctacac catgtttgtc acctggtcag 900
ccctatccag tatccctgaa cagaaatgca acccccattt gccaaaccag 950

ctgggcaacg agacagttgt ggcaggcccc gagggctatg agacccagtg 1000
 gtgggatgcc ccgagcattg tgggcctcat catcttcctc ctgtgcaccc 1050
 tcttcatcag tctgcgctcc tcagaccacc ggcaggtgaa cagcctgatg 1100
 cagaccgagg agtgcccacc tatgctagac gccacacagc agcagcagca 1150
 gcagggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200
 tcacctacag ctactccttc ttccacttct gcctgggtgct ggctcactg 1250
 cacgtcatga tgacgctcac caactggtac aagcccgggtg agacccggaa 1300
 gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350
 cagggtgct cctctacctg tggaccctgg tagccccact cctcctgcgc 1400
 aaccgcgact tcagctgagg cagcctcaca gcctgccatc tggcgcctcc 1450
 tgccacctgg tgctctcgg ctcggtgaca gccaacctgc cccctcccca 1500
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 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900
 a 1901

<210> 19

<211> 457

<212> PRT

<213> Homo sapiens

<400> 19

Met	Gly	Ala	Cys	Leu	Gly	Ala	Cys	Ser	Leu	Leu	Ser	Cys	Ala	Ser
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Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Ile	Leu	Cys	Ser	Cys	Cys	Pro
				20					25					30

Ala	Ser	Arg	Asn	Ser	Thr	Val	Ser	Arg	Leu	Ile	Phe	Thr	Phe	Phe
				35					40					45

Leu	Phe	Leu	Gly	Val	Leu	Val	Ser	Ile	Ile	Met	Leu	Ser	Pro	Gly
				50					55					60

Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly	65	70	75
Ala	Gly	Ile	Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser	80	85	90
Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala	95	100	105
Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	110	115	120
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	125	130	135
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr	140	145	150
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val	155	160	165
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile	170	175	180
Asp	Phe	Ala	His	Ser	Trp	Asn	Gln	Arg	Trp	Leu	Gly	Lys	Ala	Glu	185	190	195
Glu	Cys	Asp	Ser	Arg	Ala	Trp	Tyr	Ala	Gly	Leu	Phe	Phe	Phe	Thr	200	205	210
Leu	Leu	Phe	Tyr	Leu	Leu	Ser	Ile	Ala	Ala	Val	Ala	Leu	Met	Phe	215	220	225
Met	Tyr	Tyr	Thr	Glu	Pro	Ser	Gly	Cys	His	Glu	Gly	Lys	Val	Phe	230	235	240
Ile	Ser	Leu	Asn	Leu	Thr	Phe	Cys	Val	Cys	Val	Ser	Ile	Ala	Ala	245	250	255
Val	Leu	Pro	Lys	Val	Gln	Asp	Ala	Gln	Pro	Asn	Ser	Gly	Leu	Leu	260	265	270
Gln	Ala	Ser	Val	Ile	Thr	Leu	Tyr	Thr	Met	Phe	Val	Thr	Trp	Ser	275	280	285
Ala	Leu	Ser	Ser	Ile	Pro	Glu	Gln	Lys	Cys	Asn	Pro	His	Leu	Pro	290	295	300
Thr	Gln	Leu	Gly	Asn	Glu	Thr	Val	Val	Ala	Gly	Pro	Glu	Gly	Tyr	305	310	315
Glu	Thr	Gln	Trp	Trp	Asp	Ala	Pro	Ser	Ile	Val	Gly	Leu	Ile	Ile	320	325	330
Phe	Leu	Leu	Cys	Thr	Leu	Phe	Ile	Ser	Leu	Arg	Ser	Ser	Asp	His	335	340	345
Arg	Gln	Val	Asn	Ser	Leu	Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met			

	350		355		360
Leu Asp Ala Thr	Gln Gln Gln Gln Gln Gln	Val Ala Ala Cys Glu			
	365		370		375
Gly Arg Ala Phe	Asp Asn Glu Gln Asp	Gly Val Thr Tyr Ser Tyr			
	380		385		390
Ser Phe Phe His	Phe Cys Leu Val Leu	Ala Ser Leu His Val Met			
	395		400		405
Met Thr Leu Thr	Asn Trp Tyr Lys Pro	Gly Glu Thr Arg Lys Met			
	410		415		420
Ile Ser Thr Trp	Thr Ala Val Trp Val	Lys Ile Cys Ala Ser Trp			
	425		430		435
Ala Gly Leu Leu	Leu Tyr Leu Trp Thr	Leu Val Ala Pro Leu Leu			
	440		445		450
Leu Arg Asn Arg	Asp Phe Ser				
	455				

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 20

gccgcctcat cttcacgttc ttcc 24

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 21

tcatccagct ggtgctgctc 20

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 22

cttcttccac ttctgcctgg 20

<210> 23

<211> 18

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 23
 cctgggcaaa aatgcaac 18

 <210> 24
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 24
 caggaatgta gaaggcaccc acgg 24

 <210> 25
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 25
 tggcacagat cttcacccac acgg 24

 <210> 26
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 26
 tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

 <210> 27
 <211> 1351
 <212> DNA
 <213> Homo sapiens

 <400> 27
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 ttaacctggg tcaaatgcac ggattctcac ctcgtacagt tacgctctcc 100

 cgcggcacgt ccgcgaggac ttgaagtcc gagcgctcaa gtttgtccgt 150

 aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200

 tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250

464550

actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300
cccagagccc tattaccggg aatctggatg ggaccgcctc cgggagctgt 350
ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450
agctttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500
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cgaggcttca ttcgttatgg ctggcgctgg ggttggagaa ctgcagtgtt 600
tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650
aagatgcctt aagccatttt gtaattgcag gagctgtcac ggggaagtctt 700
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cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950
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t 1351

<210> 28
<211> 285
<212> PRT
<213> Homo sapiens

<400> 28
Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala
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Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala
20 25 30

Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val	
				35					40					45	
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu	
				50					55					60	
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala	
				65					70					75	
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val	
				80					85					90	
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile	
				95					100					105	
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val	
				110					115					120	
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly	
				125					130					135	
Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	
				140					145					150	
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	
				155					160					165	
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	
				170					175					180	
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	
				185					190					195	
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	
				200					205					210	
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	
				215					220					225	
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	
				230					235					240	
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	
				245					250					255	
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	
				260					265					270	
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	
				275					280					285	

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

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tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150
ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200
catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250
ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300
ttcgttcattg gctggcgccg aacc 324

<210> 30
<211> 377
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 262, 330, 371
<223> unknown base

<400> 30
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accgcggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100
gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150
gcggttcccc tacgtcccag agccctatta cccggaattt ggatgggacc 200
gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250
cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300
gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350
agagccaggc agaaatttat nataacc 377

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
tcgtacagtt acgctctccc 20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 32
cttgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ataacgaatg aagcctcgtg 20

<210> 34
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 34
gctaatatct gtaagacggc agctacagca ggcatcattg 40

<210> 35
<211> 1819
<212> DNA
<213> Homo sapiens

<400> 35
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ccaccacagt ctgcgttget gccccgcctg ggccaggccc caaaggcaag 100
gacaaagcag ctgtcaggga acctccgccg gagtcgaatt tacgtgcagc 150
tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200
aagaactgcc tgtgcgccct caacctgctt tacaccttg ttagtctgct 250
gctaattgga attgctgctg ggggcattgg cttcgggctg atttccagtc 300
tccgagtggc cggcgtggtc attgcagtgg gcattcttctt gttcctgatt 350
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tttttatatg attattctgt tacttgattt tattgttcag ttttctgtat 450
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gttggttgga acaatacggc aagtgtcga aatgacatcc agagaaatct 550
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gaatatgctg gagaggtttt gagatttggt ggtggcattg gcctgttctt 700

cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750
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 caatTTTTTT tgggtctttt aggaaagatt gttgtggtaa aaagtgttag 1300
 tataaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350
 ctagaaatag ttatgtctta ggaaattgtg gtttaatttt tgacttttac 1400
 aggtaagtgc aaaggagaag tggtttcatg aaatgttcta atgtataata 1450
 acatttacct tcagcctcca tcagaatgga acgagttttg agtaatcagg 1500
 aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550
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 aaaagatatt tgattatctt aaaaattgtt aaataccggt ttcatgaaat 1650
 ttctcagtat tgtaacagca acttgtaaaa cctaagcata tttgaatatg 1700
 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750
 gttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800
 taaaagaaaag taatggaag 1819

<210> 36
 <211> 204
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Val Cys Gly Gly Phe Ala Cys Ser Lys Asn Cys Leu Cys Ala
 1 5 10 15
 Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile
 20 25 30

Ala Ala Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val
35 40 45

Val Gly Val Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala
50 55 60

Leu Val Gly Leu Ile Gly Ala Val Lys His His Gln Val Leu Leu
65 70 75

Phe Phe Tyr Met Ile Ile Leu Leu Leu Val Phe Ile Val Gln Phe
80 85 90

Ser Val Ser Cys Ala Cys Leu Ala Leu Asn Gln Glu Gln Gln Gly
95 100 105

Gln Leu Leu Glu Val Gly Trp Asn Asn Thr Ala Ser Ala Arg Asn
110 115 120

Asp Ile Gln Arg Asn Leu Asn Cys Cys Gly Phe Arg Ser Val Asn
125 130 135

Pro Asn Asp Thr Cys Leu Ala Ser Cys Val Lys Ser Asp His Ser
140 145 150

Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu Tyr Ala Gly Glu Val
155 160 165

Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe Ser Phe Thr Glu
170 175 180

Ile Leu Gly Val Trp Leu Thr Tyr Arg Tyr Arg Asn Gln Lys Asp
185 190 195

Pro Arg Ala Asn Pro Ser Ala Phe Leu
200

<210> 37
<211> 390
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336
<223> unknown base

<400> 37
tgattggagc tgtaaaaaan tottcaggtg ttgtnatttt tttatatgat 50
tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttggt 100
tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tgggttgaac 150
aatacgga gtagctcgaaa tgacatccag agaaatntaa actgctgtgg 200
gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250
gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300

gagggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350

gatcctgggt gtttggctga cctacagata caggaaccag 390

<210> 38

<211> 566

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 27

<223> unknown base

<400> 38

aatcccaaat tccccaattt ttttgnctt tttagggaaa gatgtgttgt 50

ggtaaaaagt gttagtataa aaatgataat ttacttgtag tcttttatga 100

ttacaccaat gtattctaga atagttagt cttaggaaat tgtggtttaa 150

tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200

tctaattgtat aataacattt accttcagcc tcccatcaga atggaacgag 250

ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300

taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350

ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400

ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450

gcatatttga atatgatctc ccataatttg aaattgaaat cgtatttgtgt 500

ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550

gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

atgattattc tgttacttgt atttattggt cagttttatg gtatcttgcg 50

cttgtttagc ccctgaaacc aggagcaaca gggnnacagct tcttgagggt 100

tggttgga caatcacggc caagtgactc cgcaaatgac atcccagaga 150

aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200

tggtctngctg tgttaaaagt gaccactcgt gctcgccatg tgctccaatc 250

ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40

acccacgtct gcgttgctgc c 21

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 41

gagaatatgc tggagagg 18

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 42

aggaatgcac taggattcgc gcgg 24

<210> 43

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 43

ggccccaaag gcaaggacaa agcagctgtc agggaacctc cgccg 45

<210> 44

<211> 2061

<212> DNA

<213> Homo sapiens

<400> 44

cagtcaccat gaagctgggc tgtgtcctca tggcctgggc cctctacctt 50

tcccttggtg tgctctgggt ggcccagatg ctactggctg ccagttttga 100

gacgctgcag tgtgagggac ctgtctgcac tgaggagagc agctgccaca 150
 cggaggatga cttgactgat gcaagggaag ctggcttcca ggtcaaggcc 200
 tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250
 cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300
 gctgccagge ctggcaagac tggccactga ctcaggtgac cttctaccga 350
 gatggctcag ctctgggtcc ccccgggcct aacagggaat tctccatcac 400
 cgtggtacaa aaggcagaca gcgggcacta ccactgcagt ggcatcttcc 450
 agagccctgg tcttgggatc ccagaaacag catctgttgt ggctatcaca 500
 gtccaagaac tgtttccagc gccaatctc agagctgtac cctcagctga 550
 accccaagca ggaagcccca tgaccctgag ttgtcagaca aagttgcccc 600
 tgcagaggtc agctgccgc ctctcttct cttctacaa ggatggaagg 650
 atagtcaaaa gcagggggct ctctcagaa ttccagatcc ccacagcttc 700
 agaagatcac tccgggtcat actggtgtga ggcagccact gaggacaacc 750
 aagtttgaa acagagcccc cagctagaga tcagagtga gggtgcttcc 800
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 ccccatcttc tgaggatcca ggcttttctt ctctctggg gatgccagat 950
 cctcatctgt atcaccagat gggccttctt ctcaaacaca tgcaggatgt 1000
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 catccatgat ctacttaac caccccaata aatctgattc tttattttct 1150
 cttctgtcc tgcacatatg cataagtact tttacaagtt gtcccagtgt 1200
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 agaattagag ttagctata attgtgtatt ctctcttaac acaacagaat 1300
 tctgctgtct agatcaggaa tttctatctg ttatatcgac cagaatgttg 1350
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 ggggcaattt tgccccccag aggacattgg gcaatgtttg gagacatttt 1450
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ggcagtaccc cacaacgaaa aataatctgg cccaaaatgt cagttgtact 1600
 gagtttgaga aaccccagcc taatgaaacc ctaggtggtg ggctctggaa 1650
 tgggactttg tcccttctaa ttattatctc tticcagcct cattcagcta 1700
 ttcttactga cataccagtc tttagctggt gctatggtct gttctttagt 1750
 tctagtttgt atcccctcaa aagccattat gttgaaatcc taatccocaa 1800
 ggtgatggca ttaagaagtg ggcctttggg aagtgattag atcaggagtg 1850
 cagagccctc atgattagga ttagtgcctt tatttaaaaa ggccccagag 1900
 agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950
 atgagaacca aaaaacagct gtcgcaaacc accgactctg tcgttgccct 2000
 gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050
 ttgtagccta a 2061

<210> 45
 <211> 359
 <212> PRT
 <213> Homo sapiens

<400> 45
 Met Lys Leu Gly Cys Val Leu Met Ala Trp Ala Leu Tyr Leu Ser
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 Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe
 20 25 30
 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser
 35 40 45
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe
 50 55 60
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val
 65 70 75
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe
 80 85 90
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp
 95 100 105
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly
 110 115 120
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys
 125 130 135
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro
 140 145 150

Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	155	160	165
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	170	175	180
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	185	190	195
Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
tttccagcgc caattctc 18

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtcctcagtg gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

<400> 51
cccacgcgtc cgcccacgcg tccgcccacg ggtccgcca cgcgtccggg 50
ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100
gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150
gcacctaaca gtggacactt atggccgtcc catcctggaa gtgccagaga 200
gtgtaacagg accttggaag ggggatgtga atcttccttg cacctatgac 250
cccctgcaag gctacacca agtcttggtg aagtggctgg tacaacgtgg 300
ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc 350

agcaggcaaa gtaccagggc cgcctgcatg tgagccacaa ggttccagga 400
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 cacgtgtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500
 ataagattac tgagctccgt gtccagaaac tctctgtctc caagcccaca 550
 gtgacaactg gcagcgggta tggcttcacg gtgccccagg gaatgaggat 600
 tagccttcaa tgccaggctc ggggttctcc tcccatcagt tatatttggg 650
 ataagcaaca gactaataac caggaacca tcaaagtagc aaccctaagt 700
 accttactct tcaagcctgc ggtgatagcc gactcaggct cctatttctg 750
 cactgccaaag ggccagggtg gctctgagca gcacagcgac attgtgaagt 800
 ttgtggtcaa agactcctca aagctactca agaccaagac tgaggcacct 850
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 ggactggacc actgacatgg atggctacct tggagagacc agtgctgggc 950
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 ccatttttga ccccgctcct gccctcaatt ttgattactg gcaggaaatg 1150
 tggaggaagg ggggtgtggc acagaccaa tcctaaggcc ggaggccttc 1200
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 gcagaagggg gggaaaccag gaccacagcc ccaagtcctt tcttatgggt 1400
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ctttgccctg gaatttgcca gatgcatctc aagtaagcca gctgctggat 1850
 ttggctctgg gcccttctag tatctctgcc gggggcttct ggtactcctc 1900
 tctaaatacc agagggaaga tgcccatagc actaggactt ggtcatcatg 1950
 cctacagaca ctattcaact ttggcatctt gccaccagaa gacccgaggg 2000
 aggctcagct ctgccagctc agaggaccag ctatatccag gatcatttct 2050
 ctttcttcag ggccagacag cttttaattg aaattggtat ttcacaggcc 2100
 agggttcagt tctgctcctc cactataagt ctaatgttct gactctctcc 2150
 tggtgctcaa taaatatcta atcataacag c 2181

<210> 52
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val
 1 5 10 15
 Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr
 20 25 30
 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro
 35 40 45
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg
 50 55 60
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp
 65 70 75
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His
 80 85 90
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met
 95 100 105
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro
 110 115 120
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val
 125 130 135
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly
 140 145 150
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys
 155 160 165
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln
 170 175 180

Gln Thr Asn Asn	Gln Glu Pro Ile Lys	Val Ala Thr Leu Ser Thr	185	190	195
Leu Leu Phe Lys	Pro Ala Val Ile Ala	Asp Ser Gly Ser Tyr Phe	200	205	210
Cys Thr Ala Lys	Gly Gln Val Gly Ser	Glu Gln His Ser Asp Ile	215	220	225
Val Lys Phe Val	Val Lys Asp Ser Ser	Lys Leu Leu Lys Thr Lys	230	235	240
Thr Glu Ala Pro	Thr Thr Met Thr Tyr	Pro Leu Lys Ala Thr Ser	245	250	255
Thr Val Lys Gln	Ser Trp Asp Trp Thr	Thr Asp Met Asp Gly Tyr	260	265	270
Leu Gly Glu Thr	Ser Ala Gly Pro Gly	Lys Ser Leu Pro Val Phe	275	280	285
Ala Ile Ile Leu	Ile Ile Ser Leu Cys	Cys Met Val Val Phe Thr	290	295	300
Met Ala Tyr Ile	Met Leu Cys Arg Lys	Thr Ser Gln Gln Glu His	305	310	315
Val Tyr Glu Ala	Ala Arg		320		

<210> 53
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 53
 tatccctcca attgagcacc ctgg 24

 <210> 54
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 54
 gtcggaagac atcccaacaa g 21

 <210> 55
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcaqctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic oligonucleotide probe

<400> 57

tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

gcgccgggag cccatctgcc cccaggggca cggggcgcgq ggccggctcc 50

cgcccggcac atggctgcag ccacctcgcg cgcaccccga ggcgccgcgc 100

ccagctcgcc cgaggtccgt cggagggcgcc cggccgcccc ggaqccaagc 150

agcaactgag cggggaagcg cccgcgtccg gggatcggga tgtccctcct 200

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<210> 59

<211> 373

<212> PRT

<213> Homo sapiens

<400> 59

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Val	Thr	Leu	Pro	Cys	His	His	Gln	Leu	Gly	Leu	Pro	Glu	Lys	Asp	35	40	45	
Thr	Leu	Asp	Ile	Glu	Trp	Leu	Leu	Thr	Asp	Asn	Glu	Gly	Asn	Gln	50	55	60	
Lys	Val	Val	Ile	Thr	Tyr	Ser	Ser	Arg	His	Val	Tyr	Asn	Asn	Leu	65	70	75	
Thr	Glu	Glu	Gln	Lys	Gly	Arg	Val	Ala	Phe	Ala	Ser	Asn	Phe	Leu	80	85	90	
Ala	Gly	Asp	Ala	Ser	Leu	Gln	Ile	Glu	Pro	Leu	Lys	Pro	Ser	Asp	95	100	105	
Glu	Gly	Arg	Tyr	Thr	Cys	Lys	Val	Lys	Asn	Ser	Gly	Arg	Tyr	Val	110	115	120	
Trp	Ser	His	Val	Ile	Leu	Lys	Val	Leu	Val	Arg	Pro	Ser	Lys	Pro	125	130	135	
Lys	Cys	Glu	Leu	Glu	Gly	Glu	Leu	Thr	Glu	Gly	Ser	Asp	Leu	Thr	140	145	150	
Leu	Gln	Cys	Glu	Ser	Ser	Ser	Gly	Thr	Glu	Pro	Ile	Val	Tyr	Tyr	155	160	165	
Trp	Gln	Arg	Ile	Arg	Glu	Lys	Glu	Gly	Glu	Asp	Glu	Arg	Leu	Pro	170	175	180	

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Gln	Asn	Leu	Thr	Met	Ser	Tyr	Ser	Gly	Leu	Tyr	Gln	Cys	Thr	Ala	200	205	210
Gly	Asn	Glu	Ala	Gly	Lys	Glu	Ser	Cys	Val	Val	Arg	Val	Thr	Val	215	220	225
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Ile	Arg	Arg	Lys	Asp	Lys	Glu	Arg	Tyr	Glu	Glu	Glu	Glu	Arg	Pro	260	265	270
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Lys	Pro	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Arg	Ser	Ser	Arg	Ser	Gly	290	295	300
Ser	Ser	Ser	Thr	Arg	Ser	Thr	Ala	Asn	Ser	Ala	Ser	Arg	Ser	Gln	305	310	315
Arg	Thr	Leu	Ser	Thr	Asp	Ala	Ala	Pro	Gln	Pro	Gly	Leu	Ala	Thr	320	325	330
Gln	Ala	Tyr	Ser	Leu	Val	Gly	Pro	Glu	Val	Arg	Gly	Ser	Glu	Pro	335	340	345
Lys	Lys	Val	His	His	Ala	Asn	Leu	Thr	Lys	Ala	Glu	Thr	Thr	Pro	350	355	360
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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 <211> 655
 <212> PRT
 <213> Homo sapiens

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Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	
				50					55					60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	
				65					70					75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	
				80					85					90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	
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Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	
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Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	
				125					130					135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	
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Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	
				155					160					165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	
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Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	
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Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	
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Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	
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Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	
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Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	
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Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	
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Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	
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Glu	Asp	Val	Asn	Lys	Thr	Leu	Pro	Asn	Leu	Gln	Val	Val	Asn	His	
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Gln	Gln	Gly	Pro	His	His	Arg	His	Ile	Leu	Lys	Leu	Leu	Pro	Ser	
				305					310					315	
Met	Glu	Ala	Thr	Gly	Gly	Glu	Lys	Ser	Ser	Thr	Pro	Ile	Lys	Gly	

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Ile Asn Glu His 350	Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu 355	360
Val Leu Val Val 365	Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg 370	375
Thr Leu Lys Lys 380	Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu 385	390
Lys Ala Gly Leu 395	Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu 400	405
Lys Trp Ile Tyr 410	Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys 415	420
Leu Val Ala Ala 425	Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln 430	435
Phe Leu Cys Asn 440	Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn 445	450
Gly Tyr Thr Ala 455	Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His 460	465
Trp Thr Ile Arg 470	Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser 475	480
Ala Leu Arg Gln 485	His Arg Arg Asn Asp Val Val Glu Lys Ile Arg 490	495
Gly Leu Met Glu 500	Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala 505	510
Leu Pro Met Ser 515	Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser 520	525
Pro Asn Ala Lys 530	Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro 535	540
Ser Pro Gln Asp 545	Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu 550	555
Pro Leu Leu Arg 560	Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu 565	570
Ser Arg Asn Gly 575	Ser Phe Ile Thr Lys Glu Lys Lys Asp Thr Val 580	585
Leu Arg Gln Val 590	Arg Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe 595	600
Asp Asp Met Leu 605	His Phe Leu Asn Pro Glu Glu Leu Arg Val Ile 610	615

Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg Leu Phe Glu
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

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<210> 67

<211> 50

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<400> 67

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<210> 68

<211> 2412

<212> DNA

<213> Homo sapiens

<400> 68

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 <211> 453
 <212> PRT
 <213> Homo sapiens

<400> 69
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 35 40 45
 Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile
 50 55 60
 Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly
 65 70 75
 Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala
 80 85 90
 Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr
 95 100 105
 Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe

110	115	120
Thr Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly		
125	130	135
His Tyr Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr		
140	145	150
Val Ser Ser Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe		
155	160	165
Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys		
170	175	180
Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu Gly Cys Ala		
185	190	195
Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly His Arg		
200	205	210
Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu Leu		
215	220	225
Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His		
230	235	240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala		
245	250	255
Ala His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile		
260	265	270
Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His		
275	280	285
Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg		
290	295	300
Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr		
305	310	315
Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu Glu		
320	325	330
Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala		
335	340	345
Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala		
350	355	360
Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr		
365	370	375
Gly Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr		
380	385	390
Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val		
395	400	405

Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe
 410 415 420

Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg
 425 430 435

Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp
 440 445 450

Leu Lys Thr

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

tgacatcgcc cttatgaagc tggc 24

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

tacacgtccc tgtggttgca gatc 24

<210> 72

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 72

cgttcaatgc agaaatgac cagcctgtgt gcctgcccaa ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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<210> 74

<211> 735

<212> PRT

<213> Homo sapiens

<400> 74

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Leu	Ala	Leu	Ala	Gly	Ala	Leu	Leu	Ala	Pro	Cys	Glu	Ala	Arg	Gly	20	25	30	
Val	Ser	Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala	35	40	45	
Ser	Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp	50	55	60	
Ser	Lys	Asn	His	Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu	65	70	75	
Ser	Lys	Glu	Leu	Ile	Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile	80	85	90	
Ala	Ser	Ser	Phe	Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp	95	100	105	
Val	Ser	Leu	Ala	Arg	Asn	Tyr	Thr	Gly	His	Cys	Tyr	Tyr	His	Gly	110	115	120	
His	Val	Arg	Gly	Tyr	Ser	Asp	Ser	Ala	Val	Ser	Leu	Ser	Thr	Cys	125	130	135	
Ser	Gly	Leu	Arg	Gly	Leu	Ile	Val	Phe	Glu	Asn	Glu	Ser	Tyr	Val	140	145	150	
Leu	Glu	Pro	Met	Lys	Ser	Ala	Thr	Asn	Arg	Tyr	Lys	Leu	Phe	Pro	155	160	165	
Ala	Lys	Lys	Leu	Lys	Ser	Val	Arg	Gly	Ser	Cys	Gly	Ser	His	His	170	175	180	
Asn	Thr	Pro	Asn	Leu	Ala	Ala	Lys	Asn	Val	Phe	Pro	Pro	Pro	Ser	185	190	195	
Gln	Thr	Trp	Ala	Arg	Arg	His	Lys	Arg	Glu	Thr	Leu	Lys	Ala	Thr	200	205	210	

Lys Tyr Val Glu	Leu Val Ile Val Ala	Asp Asn Arg Glu Phe	Gln
215	220		225
Arg Gln Gly Lys	Asp Leu Glu Lys Val	Lys Gln Arg Leu Ile	Glu
230	235		240
Ile Ala Asn His	Val Asp Lys Phe Tyr	Arg Pro Leu Asn Ile	Arg
245	250		255
Ile Val Leu Val	Gly Val Glu Val Trp	Asn Asp Met Asp Lys	Cys
260	265		270
Ser Val Ser Gln	Asp Pro Phe Thr Ser	Leu His Glu Phe Leu	Asp
275	280		285
Trp Arg Lys Met	Lys Leu Leu Pro Arg	Lys Ser His Asp Asn	Ala
290	295		300
Gln Leu Val Ser	Gly Val Tyr Phe Gln	Gly Thr Thr Ile Gly	Met
305	310		315
Ala Pro Ile Met	Ser Met Cys Thr Ala	Asp Gln Ser Gly Gly	Ile
320	325		330
Val Met Asp His	Ser Asp Asn Pro Leu	Gly Ala Ala Val Thr	Leu
335	340		345
Ala His Glu Leu	Gly His Asn Phe Gly	Met Asn His Asp Thr	Leu
350	355		360
Asp Arg Gly Cys	Ser Cys Gln Met Ala	Val Glu Lys Gly Gly	Cys
365	370		375
Ile Met Asn Ala	Ser Thr Gly Tyr Pro	Phe Pro Met Val Phe	Ser
380	385		390
Ser Cys Ser Arg	Lys Asp Leu Glu Thr	Ser Leu Glu Lys Gly	Met
395	400		405
Gly Val Cys Leu	Phe Asn Leu Pro Glu	Val Arg Glu Ser Phe	Gly
410	415		420
Gly Gln Lys Cys	Gly Asn Arg Phe Val	Glu Glu Gly Glu Glu	Cys
425	430		435
Asp Cys Gly Glu	Pro Glu Glu Cys Met	Asn Arg Cys Cys Asn	Ala
440	445		450
Thr Thr Cys Thr	Leu Lys Pro Asp Ala	Val Cys Ala His Gly	Leu
455	460		465
Cys Cys Glu Asp	Cys Gln Leu Lys Pro	Ala Gly Thr Ala Cys	Arg
470	475		480
Asp Ser Ser Asn	Ser Cys Asp Leu Pro	Glu Phe Cys Thr Gly	Ala
485	490		495
Ser Pro His Cys	Pro Ala Asn Val Tyr	Leu His Asp Gly His	Ser

500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr	Asn Gly Ile Cys Gln Thr	
515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp	Gly Pro Gly Ala Lys Pro	
530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val	Asn Ser Ala Gly Asp Pro	
545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys	Ser Ser Phe Ala Lys Cys	
560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys	Ile Gln Cys Gln Gly Gly	
575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn	Ala Val Ser Ile Glu Thr	
590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg	Ile Leu Cys Arg Gly Thr	
605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro	Asp Pro Gly Leu Val Leu	
620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys	Ile Cys Leu Asn Arg Gln	
635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val	His Glu Cys Ala Met Gln	
650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn	Arg Lys Asn Cys His Cys	
665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys	Asp Lys Phe Gly Phe Gly	
680	685	690
Gly Ser Thr Asp Ser Gly Pro Ile Arg	Gln Ala Glu Ala Arg Gln	
695	700	705
Glu Ala Ala Glu Ser Asn Arg Glu Arg	Gly Gln Gly Gln Glu Pro	
710	715	720
Val Gly Ser Gln Glu His Ala Ser Thr	Ala Ser Leu Thr Leu Ile	
725	730	735

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 <211> 483
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> unsure
 <222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473
 <223> unknown base

 <400> 75

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 ttgagntttt tgntaaaaca tggacatgnt tcagtgtgc tcntgagaga 200
 gtagcaggtt accacttttg gcaggcccca gccctgcagc aaggaggaag 250
 aggactcaaa agtttggcct ttcactgagc ctccacagca gtgggggaga 300
 agcaaggggtt gggcccagtg tcccctttcc ccagtgcac ctcagccttg 350
 gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400
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 gagaccctgc caccattcc atntccatcc aag 483

<210> 76

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 76

gtctcagcac gtgttctggc ctcagg 27

<210> 77

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 77

catgagcatg tgcacggc 18

<210> 78

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 78

tacctgcacg atgggcac 18

<210> 79

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 79
cactgggcac ctcccttc 18

<210> 80
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
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<400> 80
ctccaggctg gtctccaagt ccttcc 26

<210> 81
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 81
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<210> 82
<211> 19
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 82
cttcgctggg aagagtttg 19

<210> 83
<211> 50
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<220>
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<400> 83
gtgcaaccaa cagatacaaa ctcttcccag cgaagaagct gaaaagcgtc 50

<210> 84
<211> 1714
<212> DNA
<213> Homo sapiens

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<211> 67
<212> PRT
<213> Homo sapiens

<400> 85
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20 25 30
Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser
35 40 45
Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
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Ala Leu Leu His Leu Tyr His
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<210> 86
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 86
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<210> 87
<211> 29
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<220>
<223> Synthetic oligonucleotide probe

<400> 87
ggtagagatg tagaaggga agcaagacc 29

<210> 88
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<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 88

gctccctacc cgtgcaggtt tcttcatttg ttcctttaac cagtatgccg 50

<210> 89

<211> 2956

<212> DNA

<213> Homo sapiens

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cgggatccag agcgcgcgcg acttcgtcat gttcttcgcg ccctggtgtg 300

gacactgcca gcggtgcag ccgacttggc atgacctggg agacaaatac 350

aacagcatgg aagatgcaa agtctatgtg gctaaagtgg actgcacggc 400

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ggtggatcag tacaaggga agcgggattt ggagtcactg agggagtacg 900

tggagtcgca gctgcagcgc acagagactg gagcgacgga gaccgtcacg 950

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<210> 90

<211> 432

<212> PRT

<213> Homo sapiens

<400> 90

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Gly	Gly	Arg	Trp	Gly	Ala	Arg	Ala	Gln	Glu	Ala	Ala	Ala	Ala	Ala	35	40	45	
Ala	Asp	Gly	Pro	Pro	Ala	Ala	Asp	Gly	Glu	Asp	Gly	Gln	Asp	Pro	50	55	60	
His	Ser	Lys	His	Leu	Tyr	Thr	Ala	Asp	Met	Phe	Thr	His	Gly	Ile	65	70	75	
Gln	Ser	Ala	Ala	His	Phe	Val	Met	Phe	Phe	Ala	Pro	Trp	Cys	Gly	80	85	90	
His	Cys	Gln	Arg	Leu	Gln	Pro	Thr	Trp	Asn	Asp	Leu	Gly	Asp	Lys	95	100	105	
Tyr	Asn	Ser	Met	Glu	Asp	Ala	Lys	Val	Tyr	Val	Ala	Lys	Val	Asp	110	115	120	
Cys	Thr	Ala	His	Ser	Asp	Val	Cys	Ser	Ala	Gln	Gly	Val	Arg	Gly	125	130	135	
Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Lys	Pro	Gly	Gln	Glu	Ala	Val	Lys	140	145	150	
Tyr	Gln	Gly	Pro	Arg	Asp	Phe	Gln	Thr	Leu	Glu	Asn	Trp	Met	Leu	155	160	165	
Gln	Thr	Leu	Asn	Glu	Glu	Pro	Val	Thr	Pro	Glu	Pro	Glu	Val	Glu	170	175	180	

Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser	
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Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile	
				200					205					210	
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	
				215					220					225	
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	
				230					235					240	
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser	
				245					250					255	
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	
				260					265					270	
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	
				275					280					285	
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly	
				290					295					300	
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	
				305					310					315	
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn	
				320					325					330	
Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	
				335					340					345	
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	
				350					355					360	
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	
				365					370					375	
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	
				380					385					390	
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	
				395					400					405	
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	
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His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<220>
<223> Synthetic oligonucleotide probe

<400> 92
ccaagccaac acactctaca g 21

<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
aagtggtcgc cttgtgcaac gtgc 24

<210> 94
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 94
ggtcaaagg gatatatgcg cac 23

<210> 95
<211> 49
<212> DNA
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<220>
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<210> 96
<211> 1016
<212> DNA
<213> Homo sapiens

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gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150

atttcaccag gacccaaagg agatgatggt gaaaaaggag atccaggaga 200
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gagaactggg tgatatggga gatcagggca atattggcaa gactggggccc 300
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aaaaaaaaa aaaaaa 1016

<210> 97
<211> 277
<212> PRT
<213> Homo sapiens

<400> 97
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Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
35 40 45
Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
50 55 60
Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
65 70 75
Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys

	80		85		90
Thr Gly Pro Ile	Gly Lys Lys Gly Asp	Lys Gly Glu Lys Gly	Leu		
	95	100	105		
Leu Gly Ile Pro	Gly Glu Lys Gly Lys	Ala Gly Thr Val Cys	Asp		
	110	115	120		
Cys Gly Arg Tyr	Arg Lys Phe Val Gly	Gln Leu Asp Ile Ser	Ile		
	125	130	135		
Ala Arg Leu Lys	Thr Ser Met Lys Phe	Val Lys Asn Val Ile	Ala		
	140	145	150		
Gly Ile Arg Glu	Thr Glu Glu Lys Phe	Tyr Tyr Ile Val Gln	Glu		
	155	160	165		
Glu Lys Asn Tyr	Arg Glu Ser Leu Thr	His Cys Arg Ile Arg	Gly		
	170	175	180		
Gly Met Leu Ala	Met Pro Lys Asp Glu	Ala Ala Asn Thr Leu	Ile		
	185	190	195		
Ala Asp Tyr Val	Ala Lys Ser Gly Phe	Phe Arg Val Phe Ile	Gly		
	200	205	210		
Val Asn Asp Leu	Glu Arg Glu Gly Gln	Tyr Met Ser Thr Asp	Asn		
	215	220	225		
Thr Pro Leu Gln	Asn Tyr Ser Asn Trp	Asn Glu Gly Glu Pro	Ser		
	230	235	240		
Asp Pro Tyr Gly	His Glu Asp Cys Val	Glu Met Leu Ser Ser	Gly		
	245	250	255		
Arg Trp Asn Asp	Thr Glu Cys His Leu	Thr Met Tyr Phe Val	Cys		
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Glu Phe Ile Lys	Lys Lys Lys				
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<210> 98

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 98

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<210> 99

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

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<223> Synthetic oligonucleotide probe

<400> 99
gatgatggag gctccatacc tcag 24

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<212> DNA
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<223> Synthetic oligonucleotide probe

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<210> 101
<211> 2574
<212> DNA
<213> Homo sapiens

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 <211> 730
 <212> PRT
 <213> Homo sapiens

<400> 102
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 Met Phe Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala
 35 40 45
 Gly Ser Met Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu
 50 55 60
 Pro Leu Leu Leu Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp
 65 70 75
 Leu Pro Ala Asp Leu Ala Phe Ala Val Arg Ala Leu Cys Cys Lys
 80 85 90
 Arg Ala Leu Arg Ala Arg Ala Leu Ala Ala Ala Ala Asp Pro
 95 100 105
 Glu Gly Pro Glu Gly Gly Cys Ser Leu Ala Trp Arg Leu Ala Glu
 110 115 120
 Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser
 125 130 135
 Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala
 140 145 150
 Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp
 155 160 165
 Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala
 170 175 180
 Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe
 185 190 195
 Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala Ala Pro
 200 205 210

Leu Ser Pro Gly	Ala Thr Val Ala	Leu Leu Leu Pro	Ala Gly Pro	215	220	225
Glu Phe Leu Trp	Leu Trp Phe Gly	Leu Ala Lys Ala	Gly Leu Arg	230	235	240
Thr Ala Phe Val	Pro Thr Ala Leu	Arg Arg Gly Pro	Leu Leu His	245	250	255
Cys Leu Arg Ser	Cys Gly Ala Arg	Ala Leu Val Leu	Ala Pro Glu	260	265	270
Phe Leu Glu Ser	Leu Glu Pro Asp	Leu Pro Ala Leu	Arg Ala Met	275	280	285
Gly Leu His Leu	Trp Ala Ala Gly	Pro Gly Thr His	Pro Ala Gly	290	295	300
Ile Ser Asp Leu	Leu Ala Glu Val	Ser Ala Glu Val	Asp Gly Pro	305	310	315
Val Pro Gly Tyr	Leu Ser Ser Pro	Gln Ser Ile Thr	Asp Thr Cys	320	325	330
Leu Tyr Ile Phe	Thr Ser Gly Thr	Thr Gly Leu Pro	Lys Ala Ala	335	340	345
Arg Ile Ser His	Leu Lys Ile Leu	Gln Cys Gln Gly	Phe Tyr Gln	350	355	360
Leu Cys Gly Val	His Gln Glu Asp	Val Ile Tyr Leu	Ala Leu Pro	365	370	375
Leu Tyr His Met	Ser Gly Ser Leu	Leu Gly Ile Val	Gly Cys Met	380	385	390
Gly Ile Gly Ala	Thr Val Val Leu	Lys Ser Lys Phe	Ser Ala Gly	395	400	405
Gln Phe Trp Glu	Asp Cys Gln Gln	His Arg Val Thr	Val Phe Gln	410	415	420
Tyr Ile Gly Glu	Leu Cys Arg Tyr	Leu Val Asn Gln	Pro Pro Ser	425	430	435
Lys Ala Glu Arg	Gly His Lys Val	Arg Leu Ala Val	Gly Ser Gly	440	445	450
Leu Arg Pro Asp	Thr Trp Glu Arg	Phe Val Arg Arg	Phe Gly Pro	455	460	465
Leu Gln Val Leu	Glu Thr Tyr Gly	Leu Thr Glu Gly	Asn Val Ala	470	475	480
Thr Ile Asn Tyr	Thr Gly Gln Arg	Gly Ala Val Gly	Arg Ala Ser	485	490	495
Trp Leu Tyr Lys	His Ile Phe Pro	Phe Ser Leu Ile	Arg Tyr Asp			

Val Thr Thr Gly	500	Pro Ile Arg Asp	505	Gln Gly His Cys Met	510
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Gln Gln Ser Pro		Phe Leu Gly Tyr Ala		Gly Gly Pro Glu Leu Ala	
545		550		555	
Gln Gly Lys Leu		Leu Lys Asp Val Phe		Arg Pro Gly Asp Val Phe	
560		565		570	
Phe Asn Thr Gly		Asp Leu Leu Val Cys		Asp Asp Gln Gly Phe Leu	
575		580		585	
Arg Phe His Asp		Arg Thr Gly Asp Thr		Phe Arg Trp Lys Gly Glu	
590		595		600	
Asn Val Ala Thr		Thr Glu Val Ala Glu		Val Phe Glu Ala Leu Asp	
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620		625		630	
Glu Gly Arg Ala		Gly Met Ala Ala Leu		Val Leu Arg Pro Pro His	
635		640		645	
Ala Leu Asp Leu		Met Gln Leu Tyr Thr		His Val Ser Glu Asn Leu	
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Ala Thr Thr Glu		Thr Phe Lys Gln Gln		Lys Val Arg Met Ala Asn	
680		685		690	
Glu Gly Phe Asp		Pro Ser Thr Leu Ser		Asp Pro Leu Tyr Val Leu	
695		700		705	
Asp Gln Ala Val		Gly Ala Tyr Leu Pro		Leu Thr Thr Ala Arg Tyr	
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<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

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<210> 104
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<400> 104
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<210> 105
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<212> DNA
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<220>
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<400> 105
gccctggcac agtgactcca tagacg 26

<210> 106
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<220>
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<400> 106
atccacttca gcggacac 18

<210> 107
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<212> DNA
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<220>
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<400> 107
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<210> 108
<211> 2579
<212> DNA
<213> Homo sapiens

<400> 108
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ccggcgcgcg ctcccacctt tgccgcacac tccggcgagc cgagcccgca 200

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<210> 109

<211> 555

<212> PRT

<213> Homo sapiens

<400> 109

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Leu	Leu	Ser	Leu	Pro	Ala	Gly	Ala	Asp	Val	Lys	Ala	Arg	Ser	Cys
				20					25					30
Gly	Glu	Val	Arg	Gln	Ala	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ala
				35					40					45
Asp	Ile	Pro	Tyr	Gln	Glu	Ile	Ala	Gly	Glu	His	Leu	Arg	Ile	Cys
				50					55					60
Pro	Gln	Glu	Tyr	Thr	Cys	Cys	Thr	Thr	Glu	Met	Glu	Asp	Lys	Leu
				65					70					75

Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150
Thr	Gly	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp	155	160	165
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Gln	Leu	Ile	Asn	Pro	Gln	Tyr	170	175	180
His	Phe	Ser	Glu	Asp	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Asp	185	190	195
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Ile	Gln	200	205	210
Val	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Arg	Thr	Phe	Val	Gln	Gly	Leu	215	220	225
Thr	Val	Gly	Arg	Glu	Val	Ala	Asn	Arg	Val	Ser	Lys	Val	Ser	Pro	230	235	240
Thr	Pro	Gly	Cys	Ile	Arg	Ala	Leu	Met	Lys	Met	Leu	Tyr	Cys	Pro	245	250	255
Tyr	Cys	Arg	Gly	Leu	Pro	Thr	Val	Arg	Pro	Cys	Asn	Asn	Tyr	Cys	260	265	270
Leu	Asn	Val	Met	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp	275	280	285
Thr	Glu	Trp	Asn	Leu	Phe	Ile	Asp	Ala	Met	Leu	Leu	Val	Ala	Glu	290	295	300
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile	305	310	315
Asp	Val	Lys	Ile	Ser	Glu	Ala	Ile	Met	Asn	Met	Gln	Glu	Asn	Ser	320	325	330
Met	Gln	Val	Ser	Ala	Lys	Val	Phe	Gln	Gly	Cys	Gly	Gln	Pro	Lys	335	340	345
Pro	Ala	Pro	Ala	Leu	Arg	Ser	Ala	Arg	Ser	Ala	Pro	Glu	Asn	Phe	350	355	360
Asn	Thr	Arg	Phe	Arg	Pro	Tyr	Asn	Pro	Glu	Glu	Arg	Pro	Thr	Thr			

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Lys Leu Lys Leu	Ser Lys Lys Val Trp	Ser Ala Leu Pro Tyr	Thr		
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Ile Cys Lys Asp	Glu Ser Val Thr Ala	Gly Thr Ser Asn Glu	Glu		
	410		415		420
Glu Cys Trp Asn	Gly His Ser Lys Ala	Arg Tyr Leu Pro Glu	Ile		
	425		430		435
Met Asn Asp Gly	Leu Thr Asn Gln Ile	Asn Asn Pro Glu Val	Asp		
	440		445		450
Val Asp Ile Thr	Arg Pro Asp Thr Phe	Ile Arg Gln Gln Ile	Met		
	455		460		465
Ala Leu Arg Val	Met Thr Asn Lys Leu	Lys Asn Ala Tyr Asn	Gly		
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Asn Asp Val Asn	Phe Gln Asp Thr Ser	Asp Glu Ser Ser Gly	Ser		
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Gly Ser Gly Ser	Gly Cys Met Asp Asp	Val Cys Pro Thr Glu	Phe		
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Glu Phe Val Thr	Thr Glu Ala Pro Ala	Val Asp Pro Asp Arg	Arg		
	515		520		525
Glu Val Asp Ser	Ser Ala Ala Gln Arg	Gly His Ser Leu Leu	Ser		
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Trp Ser Leu Thr	Cys Ile Val Leu Ala	Leu Gln Arg Leu Cys	Arg		
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 <223> Synthetic oligonucleotide probe

<400> 110
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<210> 111
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 111

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<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgcttg 40

<210> 113

<211> 4649

<212> DNA

<213> Homo sapiens

<400> 113

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cgccaactac gcaaagacca agcgggctcc gcgcggaccg gccgcggggc 150

tagggacccg gctttggcct tcaggctccc tagcagcggg gaaaaggaat 200

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ccggtccact acggcagttt atctgtctga tcagagccag acgcgacgcg 400

tccacttcgc agttctttcc aggtgtgggg accgcaggac agacggccga 450

tcccgcgcc ctccgtacca gcactcccag gagagtcagc ctcgctcccc 500

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<211> 515
<212> PRT
<213> Homo sapiens

<400> 114
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Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser
35 40 45
Trp Gly Gln Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu Leu Ala
50 55 60
Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln
65 70 75
Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp
80 85 90
Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys
95 100 105
Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro

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Ile	Cys	Thr	Pro	Ser	Arg	Ser	Gln	Phe	Ile	Thr	Gly	Lys	Tyr	Gln
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Ile	His	Thr	Gly	Leu	Gln	His	Ser	Ile	Ile	Arg	Pro	Thr	Gln	Pro
				140					145					150
Asn	Cys	Leu	Pro	Leu	Asp	Asn	Ala	Thr	Leu	Pro	Gln	Lys	Leu	Lys
				155					160					165
Glu	Val	Gly	Tyr	Ser	Thr	His	Met	Val	Gly	Lys	Trp	His	Leu	Gly
				170					175					180
Phe	Asn	Arg	Lys	Glu	Cys	Met	Pro	Thr	Arg	Arg	Gly	Phe	Asp	Thr
				185					190					195
Phe	Phe	Gly	Ser	Leu	Leu	Gly	Ser	Gly	Asp	Tyr	Tyr	Thr	His	Tyr
				200					205					210
Lys	Cys	Asp	Ser	Pro	Gly	Met	Cys	Gly	Tyr	Asp	Leu	Tyr	Glu	Asn
				215					220					225
Asp	Asn	Ala	Ala	Trp	Asp	Tyr	Asp	Asn	Gly	Ile	Tyr	Ser	Thr	Gln
				230					235					240
Met	Tyr	Thr	Gln	Arg	Val	Gln	Gln	Ile	Leu	Ala	Ser	His	Asn	Pro
				245					250					255
Thr	Lys	Pro	Ile	Phe	Leu	Tyr	Thr	Ala	Tyr	Gln	Ala	Val	His	Ser
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Pro	Leu	Gln	Ala	Pro	Gly	Arg	Tyr	Phe	Glu	His	Tyr	Arg	Ser	Ile
				275					280					285
Ile	Asn	Ile	Asn	Arg	Arg	Arg	Tyr	Ala	Ala	Met	Leu	Ser	Cys	Leu
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Asp	Glu	Ala	Ile	Asn	Asn	Val	Thr	Leu	Ala	Leu	Lys	Thr	Tyr	Gly
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Phe	Tyr	Asn	Asn	Ser	Ile	Ile	Ile	Tyr	Ser	Ser	Asp	Asn	Gly	Gly
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Gln	Pro	Thr	Ala	Gly	Gly	Ser	Asn	Trp	Pro	Leu	Arg	Gly	Ser	Lys
				335					340					345
Gly	Thr	Tyr	Trp	Glu	Gly	Gly	Ile	Arg	Ala	Val	Gly	Phe	Val	His
				350					355					360
Ser	Pro	Leu	Leu	Lys	Asn	Lys	Gly	Thr	Val	Cys	Lys	Glu	Leu	Val
				365					370					375
His	Ile	Thr	Asp	Trp	Tyr	Pro	Thr	Leu	Ile	Ser	Leu	Ala	Glu	Gly
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Gln	Ile	Asp	Glu	Asp	Ile	Gln	Leu	Asp	Gly	Tyr	Asp	Ile	Trp	Glu
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Thr Ile Ser Glu Gly Leu Arg Ser Pro Arg Val Asp Ile Leu His
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 Asn Ile Asp Pro Tyr Thr Pro Arg Gln Lys Met Ala Pro Gly Gln
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 Gln Ala Met Gly Ser Gly Thr Leu Gln Ser Ser Gln Pro Ser Glu
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 Cys Ser Thr Gly Asn Cys Leu Gln Glu Ile Leu Ala Thr Ala Thr
 455 460 465
 Gly Ser Pro Leu Ser Leu Ser Ala Thr Trp Asp Arg Thr Gly Gly
 470 475 480
 Thr Met Asn Gly Ser Pro Cys Gln Leu Ala Lys Val Tyr Gly Phe
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 Ser Thr Ser Gln Pro Thr His Met Arg Gly Trp Thr Tyr Leu Thr
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 Gly Ile Gln Glu Ser
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 115
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<210> 116
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 116
 ctctctgagt gtacatctgt gtgg 24

<210> 117
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<220>
 <221> unsure
 <222> 33
 <223> unknown base

<400> 117
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cgg 53

<210> 118
<211> 2260
<212> DNA
<213> Homo sapiens

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<223> unknown base

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tgtaccaaca gaaatattat tgtaagatgc ctttcttgta taagatatgc 1950
caatatattg tttaaatatc atatcactgt atcttctcag tcatttctga 2000
atctttccnc attatattat aaaatntgga aangtcagtt tatctcccct 2050
cctcngtata tctgatttgt atangtangt tgatgngctt ctctctacaa 2100
catttctaga aaatagaaaa aaaagcacag agaaatgttt aactgtttga 2150
ctcttatgat acttcttgga aactatgaca tcaaagatag acttttgcct 2200
aagtggctta gctgggtctt tcatagccaa acttgtatat ttaattcttt 2250
gtaataataa 2260

<210> 119
<211> 338
<212> PRT
<213> Homo sapiens

<400> 119
Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu Ser Trp
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Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly	
				20					25					30	
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	
				35					40					45	
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	
				50					55					60	
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
				65					70					75	
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	
				80					85					90	
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
				95					100					105	
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	
				110					115					120	
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	
				125					130					135	
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	
				140					145					150	
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	
				155					160					165	
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	
				170					175					180	
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
				185					190					195	
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	
				200					205					210	
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	
				215					220					225	
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	
				230					235					240	
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	
				245					250					255	
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	
				260					265					270	
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	
				275					280					285	
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
				290					295					300	
Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	

	305		310		315
Phe Asn Tyr Glu	Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly				
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Gly Lys Lys Gly	Asn Glu Glu Lys				
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<210> 120
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 120
 cctcagtggc cacatgctca tg 22

<210> 121
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 121
 ggctgcacgt atggctatcc atag 24

<210> 122
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 122
 gataaactgt cagtacagct gtgaagacac agaagaagg ccacagtgcc 50

<210> 123
 <211> 1199
 <212> DNA
 <213> Homo sapiens

<400> 123
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 ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatggtgg 150
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 gctggaaagg gtgaaaagaa gatgcctaga gaatggcaat ttaaaagaaa 300

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<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

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Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
 20 25 30

Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu
 35 40 45

Glu Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu
 50 55 60

Asp Leu Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val
 65 70 75

Leu Gln Glu Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly

80										85					90				
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr					
				95					100					105					
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr					
				110					115					120					
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile					
				125					130					135					
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser					
				140					145					150					
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn					
				155					160					165					
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser					
				170					175					180					
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser					
				185					190					195					
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln					
				200					205					210					
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile					
				215					220					225					
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro					
				230					235					240					
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala					
				245					250					255					
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe					
				260					265					270					
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys					
				275					280					285					
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<210> 125
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 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

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 gcaatgaact gggagctgc 19

 <210> 126
 <211> 19
 <212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggg atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgcc agaag 46

<210> 131

<211> 2365

<212> DNA

<213> Homo sapiens

<400> 131

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tgttacaaaa taaaa 2365

<210> 132

<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

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Ala	Trp	Ile	Leu	Phe	Phe	Val	Leu	Tyr	Asp	Phe	Cys	Ile	Val	Cys
			20						25					30

Ile	Thr	Thr	Tyr	Ala	Ile	Asn	Val	Ser	Leu	Met	Trp	Leu	Ser	Phe
			35						40					45

Arg	Lys	Val	Gln	Glu	Pro	Gln	Gly	Lys	Ala	Lys	Arg	His	Gly	Asn
			50						55					60

Thr	Val	Pro	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Val	Arg	Arg	Gln
			65						70					75

Gly	Ala	His	Ile	Cys	Ser	Gly	Ser	Leu	Val	Ala	Asp	Thr	Trp	Val	80	85	90
Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Lys	Ala	Ala	Ala	Thr	Glu	Leu	95	100	105
Asn	Ser	Trp	Ser	Val	Val	Leu	Gly	Ser	Leu	Gln	Arg	Glu	Gly	Leu	110	115	120
Ser	Pro	Gly	Ala	Glu	Glu	Val	Gly	Val	Ala	Ala	Leu	Gln	Leu	Pro	125	130	135
Arg	Ala	Tyr	Asn	His	Tyr	Ser	Gln	Gly	Ser	Asp	Leu	Ala	Leu	Leu	140	145	150
Gln	Leu	Ala	His	Pro	Thr	Thr	His	Thr	Pro	Leu	Cys	Leu	Pro	Gln	155	160	165
Pro	Ala	His	Arg	Phe	Pro	Phe	Gly	Ala	Ser	Cys	Trp	Ala	Thr	Gly	170	175	180
Trp	Asp	Gln	Asp	Thr	Ser	Asp	Ala	Pro	Gly	Thr	Leu	Arg	Asn	Leu	185	190	195
Arg	Leu	Arg	Leu	Ile	Ser	Arg	Pro	Thr	Cys	Asn	Cys	Ile	Tyr	Asn	200	205	210
Gln	Leu	His	Gln	Arg	His	Leu	Ser	Asn	Pro	Ala	Arg	Pro	Gly	Met	215	220	225
Leu	Cys	Gly	Gly	Pro	Gln	Pro	Gly	Val	Gln	Gly	Pro	Cys	Gln	Gly	230	235	240
Asp	Ser	Gly	Gly	Pro	Val	Leu	Cys	Leu	Glu	Pro	Asp	Gly	His	Trp	245	250	255
Val	Gln	Ala	Gly	Ile	Ile	Ser	Phe	Ala	Ser	Ser	Cys	Ala	Gln	Glu	260	265	270
Asp	Ala	Pro	Val	Leu	Leu	Thr	Asn	Thr	Ala	Ala	His	Ser	Ser	Trp	275	280	285
Leu	Gln	Ala	Arg	Val	Gln	Gly	Ala	Ala	Phe	Leu	Ala	Gln	Ser	Pro	290	295	300
Glu	Thr	Pro	Glu	Met	Ser	Asp	Glu	Asp	Ser	Cys	Val	Ala	Cys	Gly	305	310	315
Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	320	325	330
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	335	340	345
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	350	355	360
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly			

	365		370		375
Thr Arg Pro Glu	Glu Trp Gly Leu Lys	Gln Leu Ile Leu His	Gly		
	380		385		390
Ala Tyr Thr His	Pro Glu Gly Gly Tyr	Asp Met Ala Leu Leu	Leu		
	395		400		405
Leu Ala Gln Pro	Val Thr Leu Gly Ala	Ser Leu Arg Pro Leu	Cys		
	410		415		420
Leu Pro Tyr Pro	Asp His His Leu Pro	Asp Gly Glu Arg Gly	Trp		
	425		430		435
Val Leu Gly Arg	Ala Arg Pro Gly Ala	Gly Ile Ser Ser Leu	Gln		
	440		445		450
Thr Val Pro Val	Thr Leu Leu Gly Pro	Arg Ala Cys Ser Arg	Leu		
	455		460		465
His Ala Ala Pro	Gly Gly Asp Gly Ser	Pro Ile Leu Pro Gly	Met		
	470		475		480
Val Cys Thr Ser	Ala Val Gly Glu Leu	Pro Ser Cys Glu Gly	Leu		
	485		490		495
Ser Gly Ala Pro	Leu Val His Glu Val	Arg Gly Thr Trp Phe	Leu		
	500		505		510
Ala Gly Leu His	Ser Phe Gly Asp Ala	Cys Gln Gly Pro Ala	Arg		
	515		520		525
Pro Ala Val Phe	Thr Ala Leu Pro Ala	Tyr Glu Asp Trp Val	Ser		
	530		535		540
Ser Leu Asp Trp	Gln Val Tyr Phe Ala	Glu Glu Pro Glu Pro	Glu		
	545		550		555
Ala Glu Pro Gly	Ser Cys Leu Ala Asn	Ile Ser Gln Pro Thr	Ser		
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Cys

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- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 133
- cctgtgctgt gcctcgagcc tgac 24
- <210> 134
- <211> 24
- <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gtttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

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gatgctgctg cggcggggca gccctggcat ggggtgtgcat gtgggtgcag 200
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 catagaatct tttcttctca gacagggaca gtgcggcctc aacatctcct 1650
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 gcctctggcc agctcctggc ctctggtaga gtgagacttc agacgttctg 1850
 atgccttccg gatgtcatct ctccctgccc caggaatgga agatgtgagg 1900
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 attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137
 <211> 316
 <212> PRT
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 233
 <223> unknown amino acid

<400> 137
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Val	Gln	Val	Pro	Glu 35	Asp	Pro	Val	Val	Ala 40	Leu	Val	Gly	Thr	Asp 45	
Ala	Thr	Leu	Cys	Cys 50	Ser	Phe	Ser	Pro	Glu 55	Pro	Gly	Phe	Ser	Leu 60	
Ala	Gln	Leu	Asn	Leu 65	Ile	Trp	Gln	Leu	Thr 70	Asp	Thr	Lys	Gln	Leu 75	
Val	His	Ser	Phe	Ala 80	Glu	Gly	Gln	Asp	Gln 85	Gly	Ser	Ala	Tyr	Ala 90	
Asn	Arg	Thr	Ala	Leu 95	Phe	Pro	Asp	Leu	Leu 100	Ala	Gln	Gly	Asn	Ala 105	
Ser	Leu	Arg	Leu	Gln 110	Arg	Val	Arg	Val	Ala 115	Asp	Glu	Gly	Ser	Phe 120	
Thr	Cys	Phe	Val	Ser 125	Ile	Arg	Asp	Phe	Gly 130	Ser	Ala	Ala	Val	Ser 135	
Leu	Gln	Val	Ala	Ala 140	Pro	Tyr	Ser	Lys	Pro 145	Ser	Met	Thr	Leu	Glu 150	
Pro	Asn	Lys	Asp	Leu 155	Arg	Pro	Gly	Asp	Thr 160	Val	Thr	Ile	Thr	Cys 165	
Ser	Ser	Tyr	Gln	Gly 170	Tyr	Pro	Glu	Ala	Glu 175	Val	Phe	Trp	Gln	Asp 180	
Gly	Gln	Gly	Val	Pro 185	Leu	Thr	Gly	Asn	Val 190	Thr	Thr	Ser	Gln	Met 195	
Ala	Asn	Glu	Gln	Gly 200	Leu	Phe	Asp	Val	His 205	Ser	Val	Leu	Arg	Val 210	
Val	Leu	Gly	Ala	Asn 215	Gly	Thr	Tyr	Ser	Cys 220	Leu	Val	Arg	Asn	Pro 225	
Val	Leu	Gln	Gln	Asp 230	Ala	His	Xaa	Ser	Val 235	Thr	Ile	Thr	Gly	Gln 240	
Pro	Met	Thr	Phe	Pro 245	Pro	Glu	Ala	Leu	Trp 250	Val	Thr	Val	Gly	Leu 255	
Ser	Val	Cys	Leu	Ile 260	Ala	Leu	Leu	Val	Ala 265	Leu	Ala	Phe	Val	Cys 270	
Trp	Arg	Lys	Ile	Lys 275	Gln	Ser	Cys	Glu	Glu 280	Glu	Asn	Ala	Gly	Ala 285	
Glu	Asp	Gln	Asp	Gly 290	Glu	Gly	Glu	Gly	Ser 295	Lys	Thr	Ala	Leu	Gln 300	

Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile
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Ala

<210> 138

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 138

ctggcacagc tcaacctcat ctgg 24

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 139

gctgtctgtc tgtctcattg 20

<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 140

ggacacagta tactgaccac 20

<210> 141

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 141

tgccaaccag gcagctgtaa gtgc 24

<210> 142

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 142
tggaagaaga ggggtggtgat gtgg 24

<210> 143

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 143

cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144

<211> 2336

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1620, 1673

<223> unknown base

<400> 144

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gtttaccctg ggcatcctgg aggctctcaa aggttgggac cagggcttga 450
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gcagctacta ttgaataaat acctatcctg gatttt 2336

<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

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Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu
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Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly
35 40 45

Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly
50 55 60

Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile
65 70 75

Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln
80 85 90

Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile
95 100 105

Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro
110 115 120

Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg
125 130 135

Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn
140 145 150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys
155 160 165

Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His
170 175 180

Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys
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Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu
200 205 210

Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 146
ctttccttgc ttcagcaaca tgaggc 26

<210> 147
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 147
gcccagagca ggaggaatga tgagc 25

<210> 148
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 148
gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149
<211> 2196
<212> DNA
<213> Homo sapiens

<400> 149
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cagagatgcc tggctacctc gccctgcctt cagcctcacg gggctcagtc 200
tctttttctc tttggtgcc aaggacgga gcatggaggt cacagtacct 250
gccaccctca acgtcctcaa tggctctgac gccgcctgc cctgcacctt 300
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cgtgtgcctg taatcccagc tatttgggag gctgaggcag gagaatcgct 2100
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 tgcaattcag cctggggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 150
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 20 25 30
 Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp
 35 40 45
 Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His
 50 55 60
 Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys
 65 70 75
 Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu
 80 85 90
 Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro
 95 100 105
 Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu
 110 115 120
 Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg
 125 130 135
 His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu
 140 145 150
 Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser
 155 160 165
 Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val
 170 175 180
 Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp
 185 190 195
 Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro
 200 205 210
 Asp Asp Gly Ala Lys
 215

<210> 151

<211> 524
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 103, 233
 <223> unknown base

<400> 151
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 ccnactaaca tctcagtcgc tgaaaatgca cagagatgcc tggctacctc 150
 gccctgcctt cagcctcacg gggctcagtc tctttttctc tttggtgcc 200
 ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250
 aatggctctg acgcccgcct gccctgccct tcaactcctg ctacacagtg 300
 aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350
 ctctgaggag atgttcctcc agttccgcat gaagatcatt aacctgaagc 400
 tggagcgggt tcaagaccgc gtggagttct caggaaccc cagcaagtac 450
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 caactgctac atcatgaacc cccc 524

<210> 152
 <211> 368
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 56, 123
 <223> unknown base

<400> 152
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 ccctgaactg gatctaccag gactgcaaca actggctctg aggagatgtt 200
 cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcgggt 250
 ttcaagaacc gcgtggaagt ttctcagga acccagcaa gtacgatgtg 300
 tcggtgatgc tgagaaacgt gcagccggag gatgagggga ttacaactg 350
 ctacatcatg aaccccc 368

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acggagcatg gaggtccaca gtac 24

<210> 154
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
gcacgtttct cagcatcacc gac 23

<210> 155
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155
cgctgcct gcacctcaa ctctgtctac acagtgaacc acaaacagtt 50

<210> 156
<211> 2680
<212> DNA
<213> Homo sapiens

<400> 156
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cgcggaacca gcgtccccg ccggaagtc cccccagtg gtgctgggtcc 150
ctggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagt 200
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<210> 157
 <211> 412
 <212> PRT
 <213> Artificial

<400> 157
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 Ala Leu Pro Ala Gly Arg His Pro Pro Val Val Leu Val Pro Gly
 35 40 45
 Asp Leu Gly Asn Gln Leu Glu Ala Lys Leu Asp Lys Pro Thr Val
 50 55 60
 Val His Tyr Leu Cys Ser Lys Lys Thr Glu Ser Tyr Phe Thr Ile
 65 70 75
 Trp Leu Asn Leu Glu Leu Leu Leu Pro Val Ile Ile Asp Cys Trp
 80 85 90
 Ile Asp Asn Ile Arg Leu Val Tyr Asn Lys Thr Ser Arg Ala Thr
 95 100 105
 Gln Phe Pro Asp Gly Val Asp Val Arg Val Pro Gly Phe Gly Lys

	110		115		120
Thr Phe Ser Leu	Glu Phe Leu Asp Pro	Ser Lys Ser Ser Val	Gly		
	125		130		135
Ser Tyr Phe His	Thr Met Val Glu Ser	Leu Val Gly Trp Gly	Tyr		
	140		145		150
Thr Arg Gly Glu	Asp Val Arg Gly Ala	Pro Tyr Asp Trp Arg	Arg		
	155		160		165
Ala Pro Asn Glu	Asn Gly Pro Tyr Phe	Leu Ala Leu Arg Glu	Met		
	170		175		180
Ile Glu Glu Met	Tyr Gln Leu Tyr Gly	Gly Pro Val Val Leu	Val		
	185		190		195
Ala His Ser Met	Gly Asn Met Tyr Thr	Leu Tyr Phe Leu Gln	Arg		
	200		205		210
Gln Pro Gln Ala	Trp Lys Asp Lys Tyr	Ile Arg Ala Phe Val	Ser		
	215		220		225
Leu Gly Ala Pro	Trp Gly Gly Val Ala	Lys Thr Leu Arg Val	Leu		
	230		235		240
Ala Ser Gly Asp	Asn Asn Arg Ile Pro	Val Ile Gly Pro Leu	Lys		
	245		250		255
Ile Arg Glu Gln	Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu	Leu		
	260		265		270
Pro Tyr Asn Tyr	Thr Trp Ser Pro Glu	Lys Val Phe Val Gln	Thr		
	275		280		285
Pro Thr Ile Asn	Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe	Gln		
	290		295		300
Asp Ile Gly Phe	Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr	Glu		
	305		310		315
Gly Leu Val Glu	Ala Thr Met Pro Pro	Gly Val Gln Leu His	Cys		
	320		325		330
Leu Tyr Gly Thr	Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr	Glu		
	335		340		345
Ser Phe Pro Asp	Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly	Asp		
	350		355		360
Gly Thr Val Asn	Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp	Gln		
	365		370		375
Ser Arg Gln Glu	His Gln Val Leu Leu	Gln Glu Leu Pro Gly	Ser		
	380		385		390
Glu His Ile Glu	Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr	Leu		
	395		400		405

Lys Arg Val Leu Leu Gly Pro
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<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

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<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 160

gccccaaatg aaaacgggcc ctacttcctg gccctccgcg agatg 45

<210> 161

<211> 1512

<212> DNA

<213> Homo sapiens

<400> 161

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gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150

tcttcgcctt gatcgtgttc tcttgcatct atggtgaggg ctacagcaat 200

gccacagagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250

ctgccgctat ggcagtgcca tcgggggtgct ggccttcctg gcctcggcct 300

tcttcttggg ggtgcagcg tatttcccc agatcagcaa cgccactgac 350

cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400

cctgtggttt gttggtttct gcttcctcac caaccagtgg gcagtcacca 450
 acccgaagga cgtgctggtg ggggccgact ctgtgagggc agccatcacc 500
 ttcagcttct tttccatctt ctctggggt gtgctggcct ccctggccta 550
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 gacaactacc aacagccacc cttcaccag aacgcggaga ccaccgaggg 700
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 gtgccccatg gctcccagac tctgtctgtg ccgagtgtat tataaaatcg 1450
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 tctcattcaa ag 1512

<210> 162
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 162
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				35					40					45	
Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val	
				50					55					60	
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly	
				65					70					75	
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala	
				80					85					90	
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val	
				95					100					105	
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe	
				110					115					120	
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro	
				125					130					135	
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr	
				140					145					150	
Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly	Val	Leu	Ala	Ser	Leu	
				155					160					165	
Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp	Phe	Ile	Gln	Asn	
				170					175					180	
Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr	Ala	Ser	Tyr	
				185					190					195	
Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe	Thr	Gln	
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Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr		
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<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

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<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<400> 164
gtgtactgag cggcggtag 20

<210> 165
<211> 23
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 165
ctgaaggtga tggctgccct cac 23

<210> 166
<211> 23
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 166
ccaggaggct catgggaaag tcc 23

<210> 167
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<212> DNA
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<223> Synthetic oligonucleotide probe

<400> 167
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<210> 168
<211> 3143
<212> DNA
<213> Homo sapiens

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tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400

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tttgaataa agctgcctga tcaaaaaaaaa aaaaaaaaaa aaa 3143

<210> 169
<211> 802
<212> PRT
<213> Homo sapiens
<400> 169

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp	1	5	10	15
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Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	35	40	45	
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	50	55	60	
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	65	70	75	
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	80	85	90	
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	95	100	105	
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	110	115	120	
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly	125	130	135	
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro	140	145	150	
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu	155	160	165	
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val	170	175	180	
Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile	185	190	195	
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu	200	205	210	
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg	215	220	225	
Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	230	235	240	
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	245	250	255	
Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly	260	265	270	
Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg	275	280	285	
Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala				

				290					295					300
Val	Val	Trp	Lys	Lys	Gly	Leu	His	Ser	Tyr	Tyr	Asp	Pro	Phe	Val
				305					310					315
Leu	Ser	Val	Gln	Pro	Val	Val	Phe	Gln	Ala	Cys	Glu	Val	Asn	Leu
				320					325					330
Thr	Leu	Asp	Asn	Arg	Leu	Asp	Ser	Gln	Gly	Val	Leu	Ser	Thr	Pro
				335					340					345
Tyr	Phe	Pro	Ser	Tyr	Tyr	Ser	Pro	Gln	Thr	His	Cys	Ser	Trp	His
				350					355					360
Leu	Thr	Val	Pro	Ser	Leu	Asp	Tyr	Gly	Leu	Ala	Leu	Trp	Phe	Asp
				365					370					375
Ala	Tyr	Ala	Leu	Arg	Arg	Gln	Lys	Tyr	Asp	Leu	Pro	Cys	Thr	Gln
				380					385					390
Gly	Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu	Arg	Ile
				395					400					405
Leu	Gln	Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala	Gly
				410					415					420
Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly
				425					430					435
Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro
				440					445					450
Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys
				455					460					465
Asp	Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys
				470					475					480
Val	Cys	Arg	Ala	Thr	Phe	Gln	Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile
				485					490					495
Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly
				500					505					510
Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe
				515					520					525
Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro
				530					535					540
Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly	Ser	Asp	Glu	Glu
				545					550					555
His	Cys	Asp	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg	Ile	Val	Gly
				560					565					570
Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu
				575					580					585

Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala	Asp	
				590					595					600	
Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Gln	Glu	Asp	Ser	Met	
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Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys	Val	Trp	Gln	
				620					625					630	
Asn	Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Phe	Lys	Val	Ser	Arg	Leu	
				635					640					645	
Leu	Leu	His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His	Asp	Tyr	Asp	Val	
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Ala	Leu	Leu	Gln	Leu	Asp	His	Pro	Val	Val	Arg	Ser	Ala	Ala	Val	
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Arg	Pro	Val	Cys	Leu	Pro	Ala	Arg	Ser	His	Phe	Phe	Glu	Pro	Gly	
				680					685					690	
Leu	His	Cys	Trp	Ile	Thr	Gly	Trp	Gly	Ala	Leu	Arg	Glu	Gly	Gly	
				695					700					705	
Pro	Ile	Ser	Asn	Ala	Leu	Gln	Lys	Val	Asp	Val	Gln	Leu	Ile	Pro	
				710					715					720	
Gln	Asp	Leu	Cys	Ser	Glu	Ala	Tyr	Arg	Tyr	Gln	Val	Thr	Pro	Arg	
				725					730					735	
Met	Leu	Cys	Ala	Gly	Tyr	Arg	Lys	Gly	Lys	Lys	Asp	Ala	Cys	Gln	
				740					745					750	
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Lys	Ala	Leu	Ser	Gly	Arg	
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Trp	Phe	Leu	Ala	Gly	Leu	Val	Ser	Trp	Gly	Leu	Gly	Cys	Gly	Arg	
				770					775					780	
Pro	Asn	Tyr	Phe	Gly	Val	Tyr	Thr	Arg	Ile	Thr	Gly	Val	Ile	Ser	
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Trp	Ile	Gln	Gln	Val	Val	Thr									
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 <211> 1327
 <212> DNA
 <213> Homo sapiens

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 ggacctgtgc agcgaggcct atcgctacca ggtgacgcca cgcattgctgt 1050
 gtgccggcta ccgcaagggc aagaaggatg cctgtcaggg tgactcaggt 1100
 ggtccgctgg tgtgcaaggc actcagtggc cgctggttcc tggcggggct 1150
 ggtcagctgg ggctggggct gtggccggcc taactacttc ggcgctctaca 1200
 cccgcatcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250
 actgcccccc tgcaaagcag ggcccacctc ctggactcag agagcccagg 1300
 gcaactgcca agcaggggga caagtat 1327

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccaactgcttc cagg 24

<210> 172

<211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 172
 taatccagca gtgcaggccg gg 22

 <210> 173
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 173
 atggcctcca cgggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

 <210> 174
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 174
 tgcctatgca ctgaggaggc agaag 25

 <210> 175
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 175
 aggcaggac acagagtcca ttcac 25

 <210> 176
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 176
 agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

 <210> 177
 <211> 1510
 <212> DNA
 <213> Homo sapiens

<400> 177

ggacgagggc agatctcggt ctggggcaag ccgttgacac tcgctccctg 50
ccaccgcccg ggctccgtgc cgccaagttt tcattttcca ccttctctgc 100
ctccagtccc ccagcccctg gccgagagaa gggctcttacc ggccgggatt 150
gctggaaaca ccaagaggtg gtttttggtt tttaaaactt ctgtttcttg 200
ggaggggggtg tggcggggca ggatgagcaa ctccgttcct ctgctctgtt 250
tctggagcct ctgctattgc tttgctgcgg ggagcccgt accttttggt 300
ccagagggac ggctggaaga taagctccac aaacccaaag ctacacagac 350
tgaggtcaaa ccatctgtga ggtttaacct ccgcacctcc aaggaccag 400
agcatgaagg atgctacctc tccgtcggcc acagccagcc cttagaagac 450
tgcagtttca acatgacagc taaaaccttt ttcattcttc acggatggac 500
gatgagcggg atctttgaaa actggctgca caaactcgtg tcagccctgc 550
acacaagaga gaaagacgcc aatgtagttg tgggtgactg gctccccctg 600
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cagcattgcc aggatgctcg actggctgca ggagaaggac gatttttctc 700
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agaagtggcc agcacaatcc aatcaaatcg ttgcaaatca gattacactg 1400
tgcatgtcct aggaaaggga atctttacaa aataaacagt gtggaccct 1450

aataaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

Met	Ser	Asn	Ser	Val	Pro	Leu	Leu	Cys	Phe	Trp	Ser	Leu	Cys	Tyr
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Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg
				20					25					30

Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45

Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
				50					55					60

His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65					70					75

Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80					85					90

Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
				95					100					105

Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
				110					115					120

Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
				125					130					135

Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
				140					145					150

Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu
				155					160					165

Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn
				170					175					180

Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185					190					195

Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200					205					210

Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215					220					225

Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
				230					235					240

Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
				245					250					255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
				275					280					285
Val	Asn	Gln	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	Ser
				290					295					300
Asn	Arg	Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg
				305					310					315
Cys	Asn	Ser	Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg
				320					325					330
Asn	Ser	Lys	Met	Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg
				335					340					345
Gly	Asn	Leu	Gln	Ser	Leu	Glu	Cys	Pro						
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<210> 179
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 179
 gtgagcatga gcgagccgtc cac 23

<210> 180
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 180
 gctattacaa cgtttcttgc ggcagc 26

<210> 181
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 181
 ttgactctct ggtgaatcag gacaagcoga gttttgcctt ccag 44

<210> 182

<211> 3240
 <212> DNA
 <213> Homo sapiens

<400> 182
 cggaacgcgtg ggagggacgag tgggcctggg caagggccgg ggagccgggc 50
 cgagccacct cttccccctcc cccgcttccc tgtcgcgctc cgctggcttg 100
 acgcgctgga ggagtggagc agcaccgggc cggccctggg ggctgacagt 150
 cggcaaagt tggcccgaag aggaagtggc ctcaaaccgc ggcaggtggc 200
 gaccaggcca gaccaggggc gctcgcctgc tcgaggcggg ctgtaggcga 250
 gggcgcgccc cagtgcgag acccggggct tcaggagccg gcccgggag 300
 agaagagtgc ggagggcgac ggagaaaaca actccaaagt tggcgaaagg 350
 caccgcccct actccgggc tgcgcgcgc tccccgccc cagccctggc 400
 atccagagta cgggtcgagc ccggggccatg gagccccct ggggagggcg 450
 caccaggag cctgggcgccc cggggctccg ccgcgacccc atcgggtaga 500
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 tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150
 ctcacaaaaa gagtgaaca aatgcttcta ttccatagct acggcattgc 3200
 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met	Leu	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Ala	Leu	
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Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp
				20					25				30	
Pro	Pro	Ala	Val	Leu	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro
				35					40				45	
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu
				50					55				60	
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys
				65					70				75	
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro
				80					85				90	
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu
				95					100				105	
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly
				110					115				120	
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln
				125					130				135	
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His
				140					145				150	
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys
				155					160				165	
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro

	170		175		180
Gly Leu Thr Pro	Arg Pro Val Pro Ser	Leu Pro Cys Asn Val Thr			
	185	190			195
Leu Glu Asp Phe	Tyr Gly Val Phe Ser	Ser Pro Gly Tyr Thr His			
	200	205			210
Leu Ala Ser Val	Ser His Pro Gln Ser	Cys His Trp Leu Leu Asp			
	215	220			225
Pro His Asp Gly	Arg Arg Leu Ala Val	Arg Phe Thr Ala Leu Asp			
	230	235			240
Leu Gly Phe Gly	Asp Ala Val His Val	Tyr Asp Gly Pro Gly Pro			
	245	250			255
Pro Glu Ser Ser	Arg Leu Leu Arg Ser	Leu Thr His Phe Ser Asn			
	260	265			270
Gly Lys Ala Val	Thr Val Glu Thr Leu	Ser Gly Gln Ala Val Val			
	275	280			285
Ser Tyr His Thr	Val Ala Trp Ser Asn	Gly Arg Gly Phe Asn Ala			
	290	295			300
Thr Tyr His Val	Arg Gly Tyr Cys Leu	Pro Trp Asp Arg Pro Cys			
	305	310			315
Gly Leu Gly Ser	Gly Leu Gly Ala Gly	Glu Gly Leu Gly Glu Arg			
	320	325			330
Cys Tyr Ser Glu	Ala Gln Arg Cys Asp	Gly Ser Trp Asp Cys Ala			
	335	340			345
Asp Gly Thr Asp	Glu Glu Asp Cys Pro	Gly Cys Pro Pro Gly His			
	350	355			360
Phe Pro Cys Gly	Ala Ala Gly Thr Ser	Gly Ala Thr Ala Cys Tyr			
	365	370			375
Leu Pro Ala Asp	Arg Cys Asn Tyr Gln	Thr Phe Cys Ala Asp Gly			
	380	385			390
Ala Asp Glu Arg	Arg Cys Arg His Cys	Gln Pro Gly Asn Phe Arg			
	395	400			405
Cys Arg Asp Glu	Lys Cys Val Tyr Glu	Thr Trp Val Cys Asp Gly			
	410	415			420
Gln Pro Asp Cys	Ala Asp Gly Ser Asp	Glu Trp Asp Cys Ser Tyr			
	425	430			435
Val Leu Pro Arg	Lys Val Ile Thr Ala	Ala Val Ile Gly Ser Leu			
	440	445			450
Val Cys Gly Leu	Leu Leu Val Ile Ala	Leu Gly Cys Thr Cys Lys			
	455	460			465

Leu Tyr Ala Ile Arg Thr Gln Glu Tyr Ser Ile Phe Ala Pro Leu	470	475	480
Ser Arg Met Glu Ala Glu Ile Val Gln Gln Gln Ala Pro Pro Ser	485	490	495
Tyr Gly Gln Leu Ile Ala Gln Gly Ala Ile Pro Pro Val Glu Asp	500	505	510
Phe Pro Thr Glu Asn Pro Asn Asp Asn Ser Val Leu Gly Asn Leu	515	520	525
Arg Ser Leu Leu Gln Ile Leu Arg Gln Asp Met Thr Pro Gly Gly	530	535	540
Gly Pro Gly Ala Arg Arg Arg Gln Arg Gly Arg Leu Met Arg Arg	545	550	555
Leu Val Arg Arg Leu Arg Arg Trp Gly Leu Leu Pro Arg Thr Asn	560	565	570
Thr Pro Ala Arg Ala Ser Glu Ala Arg Ser Gln Val Thr Pro Ser	575	580	585
Ala Ala Pro Leu Glu Ala Leu Asp Gly Gly Thr Gly Pro Ala Arg	590	595	600
Glu Gly Gly Ala Val Gly Gly Gln Asp Gly Glu Gln Ala Pro Pro	605	610	615
Leu Pro Ile Lys Ala Pro Leu Pro Ser Ala Ser Thr Ser Pro Ala	620	625	630
Pro Thr Thr Val Pro Glu Ala Pro Gly Pro Leu Pro Ser Leu Pro	635	640	645
Leu Glu Pro Ser Leu Leu Ser Gly Val Val Gln Ala Leu Arg Gly	650	655	660
Arg Leu Leu Pro Ser Leu Gly Pro Pro Gly Pro Thr Arg Ser Pro	665	670	675
Pro Gly Pro His Thr Ala Val Leu Ala Leu Glu Asp Glu Asp Asp	680	685	690
Val Leu Leu Val Pro Leu Ala Glu Pro Gly Val Trp Val Ala Glu	695	700	705
Ala Glu Asp Glu Pro Leu Leu Thr	710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
ggctgtcact gtggagacac 20

<210> 185
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcaaggtcat tacagctg 18

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
agaacatagg agcagtccca ctc 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tgcttgctgc tgcacaatct cag 23

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 188
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189
<211> 663
<212> DNA
<213> Homo sapiens

<400> 189
cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100
gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150

aataaaacat cgccccttct gcttcagtgt gaaaggccac gtgaagatgc 200
tgccggtggc actaactgtg acatctatga ccttttttat catcgacaaa 250
gcccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300
atttttcata cttttatatg tactcagact tgatcgatta atgaagtggg 350
tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400
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agttgggtgga ggggtgtttg cacttgtgac agcagtatgc tgtcttgccg 500
acggggccct tatttacggg aagcttctgt tcaatcccag cggtccttac 550
cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600
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aaaaaaaaaa aaa 663

<210> 190
<211> 152
<212> PRT
<213> Homo sapiens

<400> 190
Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe
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Ser Val Lys Gly His Val Lys Met Leu Arg Leu Ala Leu Thr Val
20 25 30
Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr
35 40 45
Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile
50 55 60
Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe
65 70 75
Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe
80 85 90
Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
95 100 105
Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys
110 115 120
Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn
125 130 135
Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
140 145 150

Val Leu

<210> 191
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 212, 234, 487
<223> unknown base

<400> 191
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ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150
catcgccctt tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200
ggcactaact gngacatcta tgaccttttt tatnatcgca caagcccctg 250
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350
gcctttgctt gatattatca actcactggg aacaacagta ttcattgctca 400
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggg 450
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cgttttgcag aacctactca ggcag 25

<210> 193
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 193
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194
<211> 40

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 194
aaagtgctgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195
<211> 1879
<212> DNA
<213> Homo sapien

<400> 195
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cactggcccc ggcgctgtgt ctgcctctgc tggcccagtg gctcctgcgc 150
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 caccgctctt caatctctgt tctgtccca gatgccttct agattcactg 1800
 tcttttgatt cttgatttcc aagctttcaa atcctcccta cttccaagaa 1850
 aaataattaa aaaaaaaact tcattctaa 1879

<210> 196
 <211> 518
 <212> PRT
 <213> Homo sapien

<400> 196
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 Trp Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr
 20 25 30
 Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro
 35 40 45
 Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu
 50 55 60
 Ala Leu Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala
 65 70 75
 Asn Phe Leu Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg
 80 85 90
 Gly Tyr Tyr Leu Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu
 95 100 105

Gln Ile Leu Val	Asp Thr Gly Ser Ser	Asn Phe Ala Val Ala Gly	110	115	120
Thr Pro His Ser	Tyr Ile Asp Thr Tyr	Phe Asp Thr Glu Arg Ser	125	130	135
Ser Thr Tyr Arg	Ser Lys Gly Phe Asp	Val Thr Val Lys Tyr Thr	140	145	150
Gln Gly Ser Trp	Thr Gly Phe Val Gly	Glu Asp Leu Val Thr Ile	155	160	165
Pro Lys Gly Phe	Asn Thr Ser Phe Leu	Val Asn Ile Ala Thr Ile	170	175	180
Phe Glu Ser Glu	Asn Phe Phe Leu Pro	Gly Ile Lys Trp Asn Gly	185	190	195
Ile Leu Gly Leu	Ala Tyr Ala Thr Leu	Ala Lys Pro Ser Ser Ser	200	205	210
Leu Glu Thr Phe	Phe Asp Ser Leu Val	Thr Gln Ala Asn Ile Pro	215	220	225
Asn Val Phe Ser	Met Gln Met Cys Gly	Ala Gly Leu Pro Val Ala	230	235	240
Gly Ser Gly Thr	Asn Gly Gly Ser Leu	Val Leu Gly Gly Ile Glu	245	250	255
Pro Ser Leu Tyr	Lys Gly Asp Ile Trp	Tyr Thr Pro Ile Lys Glu	260	265	270
Glu Trp Tyr Tyr	Gln Ile Glu Ile Leu	Lys Leu Glu Ile Gly Gly	275	280	285
Gln Ser Leu Asn	Leu Asp Cys Arg Glu	Tyr Asn Ala Asp Lys Ala	290	295	300
Ile Val Asp Ser	Gly Thr Thr Leu Leu	Arg Leu Pro Gln Lys Val	305	310	315
Phe Asp Ala Val	Val Glu Ala Val Ala	Arg Ala Ser Leu Ile Pro	320	325	330
Glu Phe Ser Asp	Gly Phe Trp Thr Gly	Ser Gln Leu Ala Cys Trp	335	340	345
Thr Asn Ser Glu	Thr Pro Trp Ser Tyr	Phe Pro Lys Ile Ser Ile	350	355	360
Tyr Leu Arg Asp	Glu Asn Ser Ser Arg	Ser Phe Arg Ile Thr Ile	365	370	375
Leu Pro Gln Leu	Tyr Ile Gln Pro Met	Met Gly Ala Gly Leu Asn	380	385	390
Tyr Glu Cys Tyr	Arg Phe Gly Ile Ser	Pro Ser Thr Asn Ala Leu			

	395	400	405
Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp			
	410	415	420
Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu			
	425	430	435
Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr			
	440	445	450
Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu			
	455	460	465
Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly			
	470	475	480
Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Pro Phe Arg			
	485	490	495
Cys Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser			
	500	505	510
Ser Leu Val Arg His Arg Trp Lys			
	515		

<210> 197

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 197

cgcagaagct acagattctc g 21

<210> 198

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 198

ggaaattgga ggccaaagc 19

<210> 199

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 199

ggatgtagcc agcaactgtg 20

<210> 200
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 200
gccttggctc gttctcttc 19

<210> 201
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 201
ggtcctgtgc ctggatgg 18

<210> 202
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 202
gacaagacta cctccgttgg tc 22

<210> 203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 203
tgatgcacag ttcagcacct gttg 24

<210> 204
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 204
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205
<211> 1939
<212> DNA

<213> Homo sapiens

<400> 205

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ggggttgctg ctgggcgctt acgtgcttgt ctactacaac ctggtgaagg 200
ccccgcctgt cggcggcatg ggcaacctgc ggggcccac gccctgggtc 250
acgggcgcca acagcggcat cggaaagatg acggcgctgg agctggcgcg 300
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[illegible]

<211> 377

<213> Homo sapiens

Met Glu Ala Leu Leu Leu Gly Ala Gly Leu Leu Leu Gly Ala Tyr
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Met Gly Asn Leu Arg Gly Arg Thr Ala Val Val Thr Gly Ala Asn
35 40 45

Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala
65 70 75

Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe
95 100 105

His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe
125 130 135

140

His Leu Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val
 155 160 165
 Val Val Val Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe
 170 175 180
 Lys Arg Leu Asp Arg Pro Val Val Gly Trp Arg Gln Glu Leu Arg
 185 190 195
 Ala Tyr Ala Asp Thr Lys Leu Ala Asn Val Leu Phe Ala Arg Glu
 200 205 210
 Leu Ala Asn Gln Leu Glu Ala Thr Gly Val Thr Cys Tyr Ala Ala
 215 220 225
 His Pro Gly Pro Val Asn Ser Glu Leu Phe Leu Arg His Val Pro
 230 235 240
 Gly Trp Leu Arg Pro Leu Leu Arg Pro Leu Ala Trp Leu Val Leu
 245 250 255
 Arg Ala Pro Arg Gly Gly Ala Gln Thr Pro Leu Tyr Cys Ala Leu
 260 265 270
 Gln Glu Gly Ile Glu Pro Leu Ser Gly Arg Tyr Phe Ala Asn Cys
 275 280 285
 His Val Glu Glu Val Pro Pro Ala Ala Arg Asp Asp Arg Ala Ala
 290 295 300
 His Arg Leu Trp Glu Ala Ser Lys Arg Leu Ala Gly Leu Gly Pro
 305 310 315
 Gly Glu Asp Ala Glu Pro Asp Glu Asp Pro Gln Ser Glu Asp Ser
 320 325 330
 Glu Ala Pro Ser Ser Leu Ser Thr Pro His Pro Glu Glu Pro Thr
 335 340 345
 Val Ser Gln Pro Tyr Pro Ser Pro Gln Ser Ser Pro Asp Leu Ser
 350 355 360
 Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln
 365 370 375
 Leu Ser

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcattggcc ttggacttgg ccag 24

<210> 208
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 208
 acgccagtgg cctcaagctg gttg 24

<210> 209
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 209
 ctttctgagc tctgagccac ggttggacat cctcatccac aatgc 45

<210> 210
 <211> 3716
 <212> DNA
 <213> Homo sapiens

<400> 210
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<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

Met	Gly	Gly	Met	Ala	Gln	Asp	Ser	Pro	Pro	Gln	Ile	Leu	Val	His
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Pro	Gln	Asp	Gln	Leu	Phe	Gln	Gly	Pro	Gly	Pro	Ala	Arg	Met	Ser
				20					25					30

Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
				35					40					45

Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
				50					55					60

Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
				65					70					75

His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
				80					85					90

Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
				95					100					105

Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
				110					115					120

Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
				125					130					135

Cys	Gly	Pro	Pro	Trp	Gly	His	Pro	Glu	Pro	Thr	Val	Ser	Trp	Trp
				140					145					150

Lys	Asp	Gly	Lys	Pro	Leu	Ala	Leu	Gln	Pro	Gly	Arg	His	Thr	Val
				155					160					165

Ser	Gly	Gly	Ser	Leu	Leu	Met	Ala	Arg	Ala	Glu	Lys	Ser	Asp	Glu
				170					175					180

Gly	Thr	Tyr	Met	Cys	Val	Ala	Thr	Asn	Ser	Ala	Gly	His	Arg	Glu
				185					190					195

Ser	Arg	Ala	Ala	Arg	Val	Ser	Ile	Gln	Glu	Pro	Gln	Asp	Tyr	Thr
				200					205					210

Glu	Pro	Val	Glu	Leu	Leu	Ala	Val	Arg	Ile	Gln	Leu	Glu	Asn	Val
				215					220					225

Thr	Leu	Leu	Asn	Pro	Asp	Pro	Ala	Glu	Gly	Pro	Lys	Pro	Arg	Pro
				230					235					240

Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420
Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr	425	430	435
Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala	440	445	450
Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val	455	460	465
Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly	470	475	480
Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met	485	490	495
Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr	500	505	510
Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg	515	520	525
Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu			

530	535	540
Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro Asp		
545	550	555
Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser		
560	565	570
Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu		
575	580	585
Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp		
590	595	600
Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu		
605	610	615
Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln		
620	625	630
His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu		
635	640	645
Leu Arg Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser		
650	655	660
Gln Ser Pro Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala		
665	670	675
Leu Gly Pro Lys Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg		
680	685	690
His Leu Pro Pro Ala Pro Leu Phe Pro His Glu Thr Pro Pro Thr		
695	700	705
Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser		
710	715	720
Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys		
725	730	735
Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro		
740	745	750
Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu		
755	760	765
Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu		
770	775	780
Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro		
785	790	795
Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser		
800	805	810
Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly		
815	820	825

Gly	Val	Gly	Pro	Lys	Gly	Gly	Val	Leu	Leu	Cys	Pro	Pro	Arg	Pro	
				830					835					840	
Cys	Leu	Thr	Pro	Thr	Pro	Ser	Glu	Gly	Ser	Leu	Ala	Asn	Gly	Trp	
				845					850					855	
Gly	Ser	Ala	Ser	Glu	Asp	Asn	Ala	Ala	Ser	Ala	Arg	Ala	Ser	Leu	
				860					865					870	
Val	Ser	Ser	Ser	Asp	Gly	Ser	Phe	Leu	Ala	Asp	Ala	His	Phe	Ala	
				875					880					885	
Arg	Ala	Leu	Ala	Val	Ala	Val	Asp	Ser	Phe	Gly	Phe	Gly	Leu	Glu	
				890					895					900	
Pro	Arg	Glu	Ala	Asp	Cys	Val	Phe	Ile	Asp	Ala	Ser	Ser	Pro	Pro	
				905					910					915	
Ser	Pro	Arg	Asp	Glu	Ile	Phe	Leu	Thr	Pro	Asn	Leu	Ser	Leu	Pro	
				920					925					930	
Leu	Trp	Glu	Trp	Arg	Pro	Asp	Trp	Leu	Glu	Asp	Met	Glu	Val	Ser	
				935					940					945	
His	Thr	Gln	Arg	Leu	Gly	Arg	Gly	Met	Pro	Pro	Trp	Pro	Pro	Asp	
				950					955					960	
Ser	Gln	Ile	Ser	Ser	Gln	Arg	Ser	Gln	Leu	His	Cys	Arg	Met	Pro	
				965					970					975	
Lys	Ala	Gly	Ala	Ser	Pro	Val	Asp	Tyr	Ser						
				980					985						

<210> 212
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 212
 gaagggacct acatgtgtgt ggcc 24

<210> 213
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 213
 actgaccttc cagctgagcc acac 24

<210> 214
 <211> 50
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 214

aggactacac ggagcctgtg gagcttcttg ctgtgcgaat tcagctggaa 50

<210> 215

<211> 2749

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1869, 1887

<223> unknown base

<400> 215

ctcccacggt gtccagcgcc cagaatgcgg cttctgggtcc tgctatgggg 50
ttgcctgctg ctcccaggtt atgaagccct ggaggggccca gaggaaatca 100
gcggggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150
ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200
tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250
agggcaggggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300
accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtgggggt 350
cgaaaaacgg ggccccgatg agtctttact gatctctctg ttcgtctttc 400
caggaccctg ctgtcctccc tccccttctc ccaccttcca gcctctgggt 450
acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccagg 500
attgacttct cctggggtct acccggcagc caccacagcc aagcagggga 550
agacaggggc tgaggcccct ccattgccag ggacttcca gtacgggcac 600
gaaaggactt ctcagtacac aggaacctct cctcaccag cgacctctcc 650
tcctgcaggg agtcccgcc ccccatgca gctggactcc acctcagcag 700
aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750
atcccgatgg tccgcatact ggccccagtc ctggtgctgc tgagccttct 800
gtcagccgca ggctgatcg cttctgcag ccacctgctc ctgtggagaa 850
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ggacgtgatc tcgatgcctc ccctccacac atctgaggag gagctgggct 1000

tctcgaagtt tgtctcagcg tagggcagga ggcctcctg gccaggccag 1050
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tccccagggt ctctctttgc atgttccagc ctgacctaga agcgtttgtc 1200
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cagcagggcc agacaaggct cagtggatct ggtctgagtt tcaatctgcc 1350
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acagaagtgg ttgcctttnc catttgccct ccctggncca tgccttcttg 1900
cctttggaaa aaatgatgaa gaaaacctg gctccttcct tgtctggaaa 1950
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gagtgcacgt aggtgtctaa cacagaggag agtaggaaca gggcggatac 2050
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cctgacctca aatgagcctc ctgcttcagt ctcccaaatt gccgggatta 2400
caggcatgag ccactgtgtc tggccctatt tcctttaaaa agtgaaatta 2450

agagttgttc agtatgcaaa acttggaag atggaggaga aaaagaaaag 2500
gaagaaaaaa atgtcaccca tagtctcacc agagactatc attatttcgt 2550
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tctttttaca gagcaattat cttgtatata caactttgta tcctgccttt 2650
tccaccttat cgttccatca ctttattcca gcacttctct gtgtttttaca 2700
gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 216

<211> 332

<212> PRT

<213> Homo sapiens

<400> 216

Met	Arg	Leu	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly	1	5	10	15
Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly	20	25	30	
Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp	35	40	45	
His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg	50	55	60	
Cys	Ser	Gly	Thr	Ile	Tyr	Ala	Glu	Glu	Glu	Gly	Gln	Glu	Thr	Met	65	70	75	
Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu	80	85	90	
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr	95	100	105	
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile	110	115	120	
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser	125	130	135	
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala	140	145	150	
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu	155	160	165	
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu	170	175	180	
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr	185	190	195	
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro				

200	205	210
Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala		
215	220	225
Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg		
230	235	240
Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu		
245	250	255
Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His		
260	265	270
Leu Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln		
275	280	285
Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys		
290	295	300
Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro		
305	310	315
Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val		
320	325	330

Ser Ala

- <210> 217
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 217
- ccctgcagtg cacctacagg gaag 24
- <210> 218
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 218
- ctgtcttccc ctgcttggt gtgg 24
- <210> 219
- <211> 47
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe

<400> 219
 ggtgcaggaa ggggtgggatc ctcttctctc gctgctctgg ccacatc 47

<210> 220
 <211> 950
 <212> DNA
 <213> Homo sapiens

<400> 220
 ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50
 ggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100
 cagtgtgaaa gaaccagtgg tctcgtctctg ttgccaggc tagagtgtac 150
 tggcgtgatc atagctcact gcagcctcag actcctggac ttgagaaatc 200
 ctctctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250
 cctgtttctt ctcttctgt gagtggacca cggaggctgg tgagctgcct 300
 gtcattccaa agctcagctc tgagccagag tgggtggtggc tccacctctg 350
 ccgccggcat agaagccagg agcagggtc tcagaaggcg gtggtgcca 400
 gctgggatca tgttgttggc cctggtctgt ctgctcagct gcctgctacc 450
 ctccagttag gccaaagctct acggctcgtt tgaactggcc agagtgtac 500
 atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550
 tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600
 ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggagggt 650
 ggtgcagcaa cctcaccctg aacgtcccca acgtgtgccg gatgtactgc 700
 tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750
 gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800
 actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850
 gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900
 cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 221
 Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser
 1 5 10 15
 Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu
 20 25 30

His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp
 35 40 45
 Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala
 50 55 60
 Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln
 65 70 75
 Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro
 80 85 90
 Asn Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu
 95 100 105
 Lys Asp Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln
 110 115 120
 Gly Leu Gly Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys
 125 130 135
 Asp Leu Thr Glu Trp Val Asp Gly Cys Asp Phe
 140 145

<210> 222

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 222

gggatcatgt tgttggccct ggtc 24

<210> 223

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 223

gcaaggcaga cccagtcagc cag 23

<210> 224

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 224

ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225

<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225
agccgctgcc ccgggccggg cggccgggc ggcaccatga gtccccgctc 50
gtgcctgcgt tcgctgcgcc tctcgtctt cgcctcttc tcagccgccg 100
cgagcaactg gctgtacctg gccaaactgt cgtcgggtggg gagcatctca 150
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcagggtgca 200
gatgtgcaag cggaacctgg aagtcattga ctcgggtgcgc cgcgggtgcc 250
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300
tgctccacac tcgactcctt gccctcttc ggcaagggtg tgacgcaagg 350
gactcgggag gcggccttcg tgtacgccat ctcttcggca ggtgtggcct 400
ttgcagtgc gcgggcgtgc agcagtggg agctggagaa gtgcggctgt 450
gacaggacag tgcatggggt cagcccacag ggcttcctc ggtcaggatg 500
ctctgacaac atcgccctac gtgtggcctt ctcacagtcg tttgtggatg 550
tgccgggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600
cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650
atgcaagtgc cacggggtgt caggctcctg tgaggtaaag acgtgctggc 700
gagccgtgcc gcccttcgc cagggtgggtc acgcactgaa ggagaagttt 750
gatggtgcca ctgagggtga gccacgccgc gtgggctcct ccagggcact 800
ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850
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aaacagtctc ccaccacctc cccaagaga tactggttgt attttttgtt 1200
ctggttttgt ttttgggtcc tcatgttatt tattgccgaa accaggcagg 1250
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gctgccactg accactcagt tggtatctgt gtccgTTTT ctacttgcag 1400
 acctaagggtg gagtaacaag gagtattacc accacatggc tactgaccgt 1450
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 tacacatgga ctcttggcag cttgagccta gaagccatgt ctctcaaagt 1600
 ccctgagaaa gggaacaagc agataccagg tcaagggcac caggttcatt 1650
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 agaccacact aggcaggcat ataggctgcc atcctggacc agggatcccc 1850
 gctgtgcctt tgcagtcag cccgagtcac ctttcacagc gctgttcctc 1900
 catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950
 acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000
 ctgtgccttt gcagtcagtc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226

<211> 351

<212> PRT

<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe
1				5					10					15
Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys
				20					25					30
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys
				35					40					45
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn
				50					55					60
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile
				65					70					75
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser
				80					85					90
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly
				95					100					105
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val
				110					115					120

Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys	125	130	135
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe	140	145	150
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe	155	160	165
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser	170	175	180
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg	185	190	195
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly	200	205	210
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro	215	220	225
Pro	Phe	Arg	Gln	Val	Gly	His	Ala	Leu	Lys	Glu	Lys	Phe	Asp	Gly	230	235	240
Ala	Thr	Glu	Val	Glu	Pro	Arg	Arg	Val	Gly	Ser	Ser	Arg	Ala	Leu	245	250	255
Val	Pro	Arg	Asn	Ala	Gln	Phe	Lys	Pro	His	Thr	Asp	Glu	Asp	Leu	260	265	270
Val	Tyr	Leu	Glu	Pro	Ser	Pro	Asp	Phe	Cys	Glu	Gln	Asp	Met	Arg	275	280	285
Ser	Gly	Val	Leu	Gly	Thr	Arg	Gly	Arg	Thr	Cys	Asn	Lys	Thr	Ser	290	295	300
Lys	Ala	Ile	Asp	Gly	Cys	Glu	Leu	Leu	Cys	Cys	Gly	Arg	Gly	Phe	305	310	315
His	Thr	Ala	Gln	Val	Glu	Leu	Ala	Glu	Arg	Cys	Ser	Cys	Lys	Phe	320	325	330
His	Trp	Cys	Cys	Phe	Val	Lys	Cys	Arg	Gln	Cys	Gln	Arg	Leu	Val	335	340	345
Glu	Leu	His	Thr	Cys	Arg										350		

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 228
 tgggtgggaga ctgttttaa t t t c g g c c 28

<210> 229
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 229
 tgcttcgtca agtgccggca gtgccagcgg ctcgtggagt t 41

<210> 230
 <211> 1355
 <212> DNA
 <213> Homo sapiens

<400> 230
 cggacgcgtg ggcggacgcg tgggaggacg cgtgggaggga cgcgtgggct 50
 ggggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100
 gctccgagga ggtccccgga gggccctggg gacgctgggt gcactggagc 150
 aggagacccc tcttcttggc cctgggtgtc ctgggtcacca cagtcctttg 200
 ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gagcgcgcg 250
 cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300
 gcggcgctgg gtgccctgaa ggaggagggtc ggagactgcc acagctgctg 350
 ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400
 cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450
 cgcgtgaccc agggcttggc tgaagccggc aggggcccgtg aggacgtccg 500
 cactgagctg ttccgggcgc tggaggccgt gaggctccag aacaactcct 550
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 tgccagcgcg cacctgggtga tcgttggggg cctggatgag cagggttcc 700
 tcaactcgaa cacgcgtggc cgtggttact ggctgggcct gagggctgtg 750

cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800
cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850
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gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950
ccgcccagtg ccctggagcc gcgcccattg cagcatgtcg tctcctgggg 1000
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actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200
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gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300
gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350
aaaaa 1355

<210> 231
<211> 293
<212> PRT
<213> Homo sapiens

<400> 231
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1 5 10 15
Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg
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Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp
35 40 45
Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg
50 55 60
Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser
65 70 75
Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp
80 85 90
Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr
95 100 105
Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu
110 115 120
Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala
125 130 135

Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg	
				140					145					150	
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys	
				155					160					165	
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	
				170					175					180	
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp	
				185					190					195	
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly	
				200					205					210	
Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu	
				215					220					225	
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val	
				230					235					240	
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro	
				245					250					255	
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr	
				260					265					270	
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp	
				275					280					285	
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys								
				290											

<210> 232
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 232
 gcgagaactg tgatcatgatg ctgc 24

 <210> 233
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 233
 gtttctgaga ctcagcagcg gtgg 24

 <210> 234
 <211> 50
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

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agacaggagg aactggagcc tcattggccg gcccgggcg ccggcctcgg 200

gcttaaataag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250

cgctcccgct gtcctgccc ggtgatggaa aaccccagcc cggccgccgc 300

cctgggcaag gccctctgcg ctctcctcct ggccactctc ggcgccgccg 350

gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400

tacagcatca cttcacagg caagtggagc cagacggcct tccccaagca 450

gtaccccctg ttccgcccc ctgcgcagtg gtcttcgctg ctgggggccg 500

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<210> 236
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 236
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 35 40 45
 Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr
 50 55 60
 Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala
 65 70 75
 Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val
 80 85 90
 Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala
 95 100 105
 Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val

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His Glu Val Phe	Ser Ala Pro Ala Val	Pro Ser Gly Thr Gly Gln			
	125	130			135
Thr Ser Ala Glu	Leu Glu Val Gln Arg	Arg His Ser Leu Val Ser			
	140	145			150
Phe Val Val Arg	Ile Val Pro Ser Pro	Asp Trp Phe Val Gly Val			
	155	160			165
Asp Ser Leu Asp	Leu Cys Asp Gly Asp	Arg Trp Arg Glu Gln Ala			
	170	175			180
Ala Leu Asp Leu	Tyr Pro Tyr Asp Ala	Gly Thr Asp Ser Gly Phe			
	185	190			195
Thr Phe Ser Ser	Pro Asn Phe Ala Thr	Ile Pro Gln Asp Thr Val			
	200	205			210
Thr Glu Ile Thr	Ser Ser Ser Pro Ser	His Pro Ala Asn Ser Phe			
	215	220			225
Tyr Tyr Pro Arg	Leu Lys Ala Leu Pro	Pro Ile Ala Arg Val Thr			
	230	235			240
Leu Leu Arg Leu	Arg Gln Ser Pro Arg	Ala Phe Ile Pro Pro Ala			
	245	250			255
Pro Val Leu Pro	Ser Arg Asp Asn Glu	Ile Val Asp Ser Ala Ser			
	260	265			270
Val Pro Glu Thr	Pro Leu Asp Cys Glu	Val Ser Leu Trp Ser Ser			
	275	280			285
Trp Gly Leu Cys	Gly Gly His Cys Gly	Arg Leu Gly Thr Lys Ser			
	290	295			300
Arg Thr Arg Tyr	Val Arg Val Gln Pro	Ala Asn Asn Gly Ser Pro			
	305	310			315
Cys Pro Glu Leu	Glu Glu Glu Ala Glu	Cys Val Pro Asp Asn Cys			
	320	325			330

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcactgcc aggggaagag gg 22

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<210> 238
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 238
caggactcgc tacgtccg 18

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
cagccccttc tcctcctttc tccc 24

<210> 240
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 240
gcagttatca gggacgcact cagcc 25

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 241
ccagcgagag gcagatag 18

<210> 242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
cggtcaccgt gtccctgcggg atg 23

<210> 243
<211> 42
<212> DNA

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 243

cagccccttc tcctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

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tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagcttg 300
cagaaaat ttt atccaacttt gtttggaagc ttattatgac aataccattt 350
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tcattcacgg ttgcgtttta atcggagagg actggttgcc atggcaaag 500
ctggtttctca tgataatggc agccagtttt tcttcacact gggtcgagca 550
gatgaactta acaataagca taccatcttt ggaaagggtta caggggatac 600
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atgcaccaga tttagttgat gatggagaag atgaaagtgc agagcatgat 1000
gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgcca 1050
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tgcagcaaaa caagcagaaa aaagaagtga agaggaagaa gccctccag 1250
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catgtgtttt ttcttagctg accttttata ttgctaaatc tgaaataaaa 1850
taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245

<211> 472

<212> PRT

<213> Homo sapiens

<400> 245

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Leu	Leu	Lys	Thr	Thr	Ala	Gly	Asp	Ile	Asp	Ile	Glu	Leu	Trp	Ser
			20					25						30
Lys	Glu	Ala	Pro	Lys	Ala	Cys	Arg	Asn	Phe	Ile	Gln	Leu	Cys	Leu
			35					40						45
Glu	Ala	Tyr	Tyr	Asp	Asn	Thr	Ile	Phe	His	Arg	Val	Val	Pro	Gly
			50					55						60
Phe	Ile	Val	Gln	Gly	Gly	Asp	Pro	Thr	Gly	Thr	Gly	Ser	Gly	Gly
			65					70						75
Glu	Ser	Ile	Tyr	Gly	Ala	Pro	Phe	Lys	Asp	Glu	Phe	His	Ser	Arg
			80					85						90
Leu	Arg	Phe	Asn	Arg	Arg	Gly	Leu	Val	Ala	Met	Ala	Asn	Ala	Gly
			95					100						105

Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala	
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Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly	
				125					130					135	
Asp	Thr	Val	Tyr	Asn	Met	Leu	Arg	Leu	Ser	Glu	Val	Asp	Ile	Asp	
				140					145					150	
Asp	Asp	Glu	Arg	Pro	His	Asn	Pro	His	Lys	Ile	Lys	Ser	Cys	Glu	
				155					160					165	
Val	Leu	Phe	Asn	Pro	Phe	Asp	Asp	Ile	Ile	Pro	Arg	Glu	Ile	Lys	
				170					175					180	
Arg	Leu	Lys	Lys	Glu	Lys	Pro	Glu	Glu	Glu	Val	Lys	Lys	Leu	Lys	
				185					190					195	
Pro	Lys	Gly	Thr	Lys	Asn	Phe	Ser	Leu	Leu	Ser	Phe	Gly	Glu	Glu	
				200					205					210	
Ala	Glu	Glu	Glu	Glu	Glu	Glu	Val	Asn	Arg	Val	Ser	Gln	Ser	Met	
				215					220					225	
Lys	Gly	Lys	Ser	Lys	Ser	Ser	His	Asp	Leu	Leu	Lys	Asp	Asp	Pro	
				230					235					240	
His	Leu	Ser	Ser	Val	Pro	Val	Val	Glu	Ser	Glu	Lys	Gly	Asp	Ala	
				245					250					255	
Pro	Asp	Leu	Val	Asp	Asp	Gly	Glu	Asp	Glu	Ser	Ala	Glu	His	Asp	
				260					265					270	
Glu	Tyr	Ile	Asp	Gly	Asp	Glu	Lys	Asn	Leu	Met	Arg	Glu	Arg	Ile	
				275					280					285	
Ala	Lys	Lys	Leu	Lys	Lys	Asp	Thr	Ser	Ala	Asn	Val	Lys	Ser	Ala	
				290					295					300	
Gly	Glu	Gly	Glu	Val	Glu	Lys	Lys	Ser	Val	Ser	Arg	Ser	Glu	Glu	
				305					310					315	
Leu	Arg	Lys	Glu	Ala	Arg	Gln	Leu	Lys	Arg	Glu	Leu	Leu	Ala	Ala	
				320					325					330	
Lys	Gln	Lys	Lys	Val	Glu	Asn	Ala	Ala	Lys	Gln	Ala	Glu	Lys	Arg	
				335					340					345	
Ser	Glu	Glu	Glu	Glu	Ala	Pro	Pro	Asp	Gly	Ala	Val	Ala	Glu	Tyr	
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Arg	Arg	Glu	Lys	Gln	Lys	Tyr	Glu	Ala	Leu	Arg	Lys	Gln	Gln	Ser	
				365					370					375	
Lys	Lys	Gly	Thr	Ser	Arg	Glu	Asp	Gln	Thr	Leu	Ala	Leu	Leu	Asn	
				380					385					390	
Gln	Phe	Lys	Ser	Lys	Leu	Thr	Gln	Ala	Ile	Ala	Glu	Thr	Pro	Glu	

395	400	405
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410	415	420
Ser His Val Leu Gln Phe Glu Asp Lys	Ser Arg Lys Val Lys Asp	
425	430	435
Ala Ser Met Gln Asp Ser Asp Thr Phe	Glu Ile Tyr Asp Pro Arg	
440	445	450
Asn Pro Val Asn Lys Arg Arg Arg Glu	Glu Ser Lys Lys Leu Met	
455	460	465
Arg Glu Lys Lys Glu Arg Arg		
470		

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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cagatggtgc tgttgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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caactggaac aggaactgag atgtggatc 29

<210> 250

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 250

ctggttcagc agtgcaaggg tctg 24

<210> 251

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 251

cctctccgat taaaacgc 18

<210> 252

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 252

gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253

<211> 2456

<212> DNA

<213> Homo sapiens

<400> 253

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ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgccggcgg 200

gaccagcaca ggcggcggtt tctccttcgg aacgggaacg tctagcaacc 250

cttctgtggg gctcaatttt ggaaatcttg gaagtacttc aactccagca 300

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 tcttatggga ggtcgacca gactgccact gcccctgtca ctgcaccag 2250
 cttggcattt accatccatc ctgctcaacc ttgttcctgt ctgttcacat 2300
 tggcctggag gcctagggca ggttgtgaca tggagcaaac ttttgtagt 2350
 ttgggatctt ctctccacc cacacttatc tccccaggg cactccaaa 2400
 gtctatacac aggggtgggc tcttcaataa agaagtgttg attagaaaaa 2450
 aaaaaa 2456

<210> 254
 <211> 545
 <212> PRT
 <213> Homo sapiens

<400> 254
 Met Ser Thr Gly Phe Ser Phe Gly Ser Gly Thr Leu Gly Ser Thr
 1 5 10 15
 Thr Val Ala Ala Gly Gly Thr Ser Thr Gly Gly Val Phe Ser Phe
 20 25 30
 Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly
 35 40 45
 Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser
 50 55 60
 Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly
 65 70 75
 Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg
 80 85 90
 Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
 95 100 105
 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe
 110 115 120
 Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro
 125 130 135

Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro	
				140					145					150	
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	
				155					160					165	
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	
				170					175					180	
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	
				185					190					195	
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	
				200					205					210	
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	
				215					220					225	
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	
				230					235					240	
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	
				245					250					255	
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	
				260					265					270	
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	
				275					280					285	
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	
				290					295					300	
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	
				305					310					315	
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	
				320					325					330	
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	
				335					340					345	
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	
				350					355					360	
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	
				365					370					375	
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	
				380					385					390	
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	
				395					400					405	
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	
				410					415					420	
Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro	Asp	Asp	Pro	

425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val	Ser Ser Val Pro Tyr Leu	
440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn	Trp Leu Leu Pro Tyr Asn	
455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val	Val Glu Glu Tyr Leu Asp	
470	475	480
Asn Val Asn Glu His Asp Trp Lys Met	Leu Arg Asn Arg Met Met	
485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val	Tyr Ala Thr Leu Gln Thr	
500	505	510
Ala His Tyr His Arg Glu Thr Pro Met	Met Gly Ile Cys Pro Ala	
515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser	Thr Cys Ser Trp Ile Leu	
530	535	540
Pro Gln Glu Trp Ala		
545		

<210> 255
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 255
 aggtgcctgc aggagtcctg ggg 23

<210> 256
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 256
 ccacctcagg aagccgaaga tgcc 24

<210> 257
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 257
 gaacggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258
<211> 2764
<212> DNA
<213> Homo sapiens

<400> 258
gagaacaggc ctgtctcagg caggccctgc gcctcctatg cggagatgct 50
actgccactg ctgctgtcct cgctgctggg cgggtcccag gctatggatg 100
ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150
tgcatctctg tgccctgctc tttctcctac ccccgacaag actggacagg 200
gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250
aggggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300
acccggggcc gattccagct cactggggat cccgccaagg ggaactgctc 350
cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttctttc 400
gggtggagag aggaagctat gtgacatata atttcatgaa cgatgggttc 450
tttctaaaag taacagtgtc cagcttcacg cccagacccc aggaccacaa 500
caccgacctc acctgccatg tggacttctc cagaaagggg gtgagcgcac 550
agaggaccgt ccgactccgt gtggcctatg ccccagaga ccttgttatc 600
agcatttcac gtgacaacac gccagccctg gagccccagc cccagggaaa 650
tgtcccatac ctggaagccc aaaaaggcca gttcctgcgg ctctctgtgtg 700
ctgctgacag ccagccccct gccacactga gctgggtcct gcagaacaga 750
gtcctctcct cgtcccatcc ctggggccct agaccctgg ggctggagct 800
gcccgggggtg aaggctgggg attcagggcg ctacacctgc cgagcggaga 850
acaggcttgg ctcccagcag cgagccctgg acctctctgt gcagtatcct 900
ccagagaacc tgagagtgat ggtttcccaa gcaaacagga cagtcctgga 950
aaaccttggg aacggcacgt ctctcccagt actggagggc caaagcctgt 1000
gcctgggtctg tgtcacacac agcagcccc cagccaggct gagctggacc 1050
cagaggggac aggttctgag cccctcccag cctcagacc ccggggtcct 1100
ggagctgcct cgggttcaag tggagcacga aggagagttc acctgccacg 1150
ctoggcacc actgggctcc cagcacgtct ctctcagcct ctccgtgcac 1200
tataagaagg gactcatctc aacggcattc tccaacggag cgtttctggg 1250
aatcggcatc acggctcttc ttttctctg cctggccctg atcatcatga 1300

agattctacc gaagagacgg actcagacag aaaccccgag gccaggttc 1350
 tcccggcaca gcacgatcct ggattacatc aatgtggtcc cgacggctgg 1400
 cccoctgggt cagaagcgga atcagaaagc cacaccaaac agtcctcgga 1450
 cccctcctcc accaggtgct ccctccccag aatcaaagaa gaaccagaaa 1500
 aagcagtatc agttgccag tttcccagaa cccaaatcat ccaactcaagc 1550
 cccagaatcc caggagagcc aagaggagct ccattatgcc acgctcaact 1600
 tcccaggcgt cagaccagc cctgaggccc ggatgcccac gggcaccag 1650
 gcggattatg cagaagtcaa gttccaatga gggctcttta ggcttttagga 1700
 ctgggacttc ggctagggag gaaggtagag taagaggttg aagataacag 1750
 agtgcaaagt ttctttctct ccctctctct ctctctttct ctctctctct 1800
 ctctttctct ctcttttaaa aaaacatctg gccagggcac agtggctcac 1850
 gcctgtaatc ccagcacttt gggaggttga ggtgggcaga tcgcctgagg 1900
 tcgggagttc gagaccagcc tggccaactt ggtgaaacc cgtctctact 1950
 aaaaatacaa aaattagctg ggcatggtgg caggcgctg taatcctacc 2000
 tacttgaggaa gctgaggcag gagaatcact tgaacctggg agacggaggt 2050
 tgcagtgagc caagatcaca ccattgcacg ccagcctggg caacaaagcg 2100
 agactccatc tcaaaaaaaaa aatcctccaa atgggttggg tgtctgtaat 2150
 cccagcactt tgggaggcta aggtgggtgg attgcttgag cccaggagtt 2200
 cgagaccagc ctgggcaaca tggtgaaacc ccctctctac aaaaaataca 2250
 aaacatagct gggcttggtg gtgtgtgcct gtagtcccag ctgtcagaca 2300
 tttaaaccag agcaactcca tctggaatag gagctgaata aaatgaggct 2350
 gagacctact gggctgcatt ctgagacagt ggaggcattc taagtcacag 2400
 gatgagacag gaggtccgta caagatacag gtcataaaga ctttgctgat 2450
 aaaacagatt gcagtaaaga agccaaccaa atcccaccaa aaccaagttg 2500
 gccacgagag tgacctctgg tcgtcctcac tgctacactc ctgacagcac 2550
 catgacagtt tacaaatgcc atggcaacat caggaagtta cccgatatgt 2600
 cccaaaaggg ggaggaatga ataatccacc ccttgtttag caaataagca 2650
 agaaataacc ataaaagtgg gcaaccagca gctctaggcg ctgctcttgt 2700
 ctatggagta gccattcttt tgttccttta ctttcttaat aaacttgctt 2750

Lys	Ala	Gly	Asp	Ser	Gly	Arg	Tyr	Thr	Cys	Arg	Ala	Glu	Asn	Arg	
				260					265					270	
Leu	Gly	Ser	Gln	Gln	Arg	Ala	Leu	Asp	Leu	Ser	Val	Gln	Tyr	Pro	
				275					280					285	
Pro	Glu	Asn	Leu	Arg	Val	Met	Val	Ser	Gln	Ala	Asn	Arg	Thr	Val	
				290					295					300	
Leu	Glu	Asn	Leu	Gly	Asn	Gly	Thr	Ser	Leu	Pro	Val	Leu	Glu	Gly	
				305					310					315	
Gln	Ser	Leu	Cys	Leu	Val	Cys	Val	Thr	His	Ser	Ser	Pro	Pro	Ala	
				320					325					330	
Arg	Leu	Ser	Trp	Thr	Gln	Arg	Gly	Gln	Val	Leu	Ser	Pro	Ser	Gln	
				335					340					345	
Pro	Ser	Asp	Pro	Gly	Val	Leu	Glu	Leu	Pro	Arg	Val	Gln	Val	Glu	
				350					355					360	
His	Glu	Gly	Glu	Phe	Thr	Cys	His	Ala	Arg	His	Pro	Leu	Gly	Ser	
				365					370					375	
Gln	His	Val	Ser	Leu	Ser	Leu	Ser	Val	His	Tyr	Lys	Lys	Gly	Leu	
				380					385					390	
Ile	Ser	Thr	Ala	Phe	Ser	Asn	Gly	Ala	Phe	Leu	Gly	Ile	Gly	Ile	
				395					400					405	
Thr	Ala	Leu	Leu	Phe	Leu	Cys	Leu	Ala	Leu	Ile	Ile	Met	Lys	Ile	
				410					415					420	
Leu	Pro	Lys	Arg	Arg	Thr	Gln	Thr	Glu	Thr	Pro	Arg	Pro	Arg	Phe	
				425					430					435	
Ser	Arg	His	Ser	Thr	Ile	Leu	Asp	Tyr	Ile	Asn	Val	Val	Pro	Thr	
				440					445					450	
Ala	Gly	Pro	Leu	Ala	Gln	Lys	Arg	Asn	Gln	Lys	Ala	Thr	Pro	Asn	
				455					460					465	
Ser	Pro	Arg	Thr	Pro	Pro	Pro	Pro	Gly	Ala	Pro	Ser	Pro	Glu	Ser	
				470					475					480	
Lys	Lys	Asn	Gln	Lys	Lys	Gln	Tyr	Gln	Leu	Pro	Ser	Phe	Pro	Glu	
				485					490					495	
Pro	Lys	Ser	Ser	Thr	Gln	Ala	Pro	Glu	Ser	Gln	Glu	Ser	Gln	Glu	
				500					505					510	
Glu	Leu	His	Tyr	Ala	Thr	Leu	Asn	Phe	Pro	Gly	Val	Arg	Pro	Arg	
				515					520					525	
Pro	Glu	Ala	Arg	Met	Pro	Lys	Gly	Thr	Gln	Ala	Asp	Tyr	Ala	Glu	
				530					535					540	
Val	Lys	Phe	Gln												

<210> 260
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 260
 caaagcctgc gcctgggtctg tg 22

<210> 261
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 261
 ttctggagcc cagaggggtgc tgag 24

<210> 262
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 262
 ggagctgccca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263
 <211> 2857
 <212> DNA
 <213> Homo sapiens

<400> 263
 tgaagagtaa tagttggaat caaaagagtc aacgcaatga actggttattt 50
 actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100
 caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150
 ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200
 aatgaatacg actagtcatc acatcggcca gctaagatct gatttagaca 250
 atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300
 acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350
 tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400
 tcgctactgg aagggctgtg gaacctgagt ctgagtttgt catcaaagtt 450

gaaaacagat tctatttcct gagaaaagtg aagatttcag agagaatata 1950
 ttccaatatg atgatgaagg gggtaggagaa gaagatacag aggcctttga 2000
 tatagcagag ctgaggagta gtaccataat gcgggaacgc aagactcgga 2050
 aaaccacaag cgctgagatc aggagcctat acaggcagtc tttgcaagtt 2100
 ggccccgaca gtgccatatt caggaaattc attctggaaa agctcgaaga 2150
 agctaatact gatccgtgtg cccctccttt tgattccctc cagacctacg 2200
 cttttgaggg aacaggggtca ttagctggat ccctgagctc cttagaatca 2250
 gcagtctctg atcaggatga aagctatgat taccttaatg agttgggacc 2300
 tcgcttttaa agattagcat gcatgtttgg ttctgcagtg cagtcaaata 2350
 attagggctt ttaccatca aaatttttaa aagtgctaata gtgtattcga 2400
 acccaatggt agtcttaaag agttttgtgc cctggctcta tggcggggaa 2450
 agccctagtc tatggagttt tctgatttcc ctggagtaaa tactccatgg 2500
 ttattttaag ctacctacat gctgtcattg aacagagatg tggggagaaa 2550
 tgtaaacaat cagctcacag gcatcaatac aaccagattt gaagtaaaat 2600
 aatgtaggaa gatattaaaa gtagatgaga ggacacaaga tgtagtcgat 2650
 ccttatgcga ttatatcatt atttacttag gaaagagtaa aaataccaaa 2700
 cgagaaaatt taaaggagca aaaatttgca agtcaaataag aaatgtacaa 2750
 atcgagataa catttacatt tctatcatat tgacatgaaa attgaaaatg 2800
 tatagtcaga gaaattttca tgaattattc catgaagtat tgtttccttt 2850
 atttaaa 2857

<210> 264
 <211> 772
 <212> PRT
 <213> Homo sapiens

<400> 264
 Met Asn Cys Tyr Leu Leu Leu Arg Phe Met Leu Gly Ile Pro Leu
 1 5 10 15
 Leu Trp Pro Cys Leu Gly Ala Thr Glu Asn Ser Gln Thr Lys Lys
 20 25 30
 Val Lys Gln Pro Val Arg Ser His Leu Arg Val Lys Arg Gly Trp
 35 40 45
 Val Trp Asn Gln Phe Phe Val Pro Glu Glu Met Asn Thr Thr Ser
 50 55 60

Val	Glu	Asp	Val	Asp	Glu	Pro	Pro	Leu	Phe	Leu	Leu	Pro	Tyr	Tyr		350	355	360
				365					370					375				
Val	Phe	Glu	Val	Phe	Glu	Glu	Thr	Pro	Gln	Gly	Ser	Phe	Val	Gly				
				380					385					390				
Val	Val	Ser	Ala	Thr	Asp	Pro	Asp	Asn	Arg	Lys	Ser	Pro	Ile	Arg				
				395					400					405				
Tyr	Ser	Ile	Thr	Arg	Ser	Lys	Val	Phe	Asn	Ile	Asn	Asp	Asn	Gly				
				410					415					420				
Thr	Ile	Thr	Thr	Ser	Asn	Ser	Leu	Asp	Arg	Glu	Ile	Ser	Ala	Trp				
				425					430					435				
Tyr	Asn	Leu	Ser	Ile	Thr	Ala	Thr	Glu	Lys	Tyr	Asn	Ile	Glu	Gln				
				440					445					450				
Ile	Ser	Ser	Ile	Pro	Leu	Tyr	Val	Gln	Val	Leu	Asn	Ile	Asn	Asp				
				455					460					465				
His	Ala	Pro	Glu	Phe	Ser	Gln	Tyr	Tyr	Glu	Thr	Tyr	Val	Cys	Glu				
				470					475					480				
Asn	Ala	Gly	Ser	Gly	Gln	Val	Ile	Gln	Thr	Ile	Ser	Ala	Val	Asp				
				485					490					495				
Arg	Asp	Glu	Ser	Ile	Glu	Glu	His	His	Phe	Tyr	Phe	Asn	Leu	Ser				
				500					505					510				
Val	Glu	Asp	Thr	Asn	Asn	Ser	Ser	Phe	Thr	Ile	Ile	Asp	Asn	Gln				
				515					520					525				
Asp	Asn	Thr	Ala	Val	Ile	Leu	Thr	Asn	Arg	Thr	Gly	Phe	Asn	Leu				
				530					535					540				
Gln	Glu	Glu	Pro	Val	Phe	Tyr	Ile	Ser	Ile	Leu	Ile	Ala	Asp	Asn				
				545					550					555				
Gly	Ile	Pro	Ser	Leu	Thr	Ser	Thr	Asn	Thr	Leu	Thr	Ile	His	Val				
				560					565					570				
Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln				
				575					580					585				
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala				
				590					595					600				
Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr				
				605					610					615				
Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys				
				620					625					630				
Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly				
				635					640					645				

Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg
				650					655					660
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser
				665					670					675
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro
				680					685					690
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu
				695					700					705
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr
				710					715					720
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser
				725					730					735
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu
				740					745					750
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly
				755					760					765
Ser	Ala	Val	Gln	Ser	Asn	Asn								
				770										

<210> 265
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 24, 60, 141, 226, 228, 249, 252
 <223> unknown base

<400> 265
 atttcaaggc cagccatatt tttntggtga accaacaaca ggagtcataa 50
 gaatatatttn taaaatggat agagaactgc aagatgagta ttgggtaatc 100
 attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150
 aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200
 aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
 tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
 aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg caccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

gcaacctcag cttctagtat ccagactcca gcgccgcccc gggcgcgagc 50

cccaaccccc acccagagct tctccagcgg cgccgcagcg agcagggctc 100

cccgcccttaa cttcctccgc ggggcccage caccttcggg agtccggggtt 150

gccacctgc aaactctccg ctttctgcac ctgccacccc tgagccagcg 200

cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250

cattctcgcc ttcttgggat ggatcgggcg catcgtcagc actgccctgc 300

cccagtggag gatttactcc tatgccggcg acaacatcgt gaccgcccag 350

gcatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400

gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450

aagcaacccg tgccttgatg gtggttggca tcctcctggg agtgatagca 500

atctttgtgg ccaccgttgg catgaagtgt atgaagtgct tggaagacga 550

tgagggtgcag aagatgagga tggctgtcat tgggggtgcg atatttcttc 600

ttgcaggctct ggctatittta gttgccacag catggtatgg caatagaatc 650
 gttcaagaat tctatgaccc tatgacccca gtcaatgcca ggtacgaatt 700
 tggtcaggct ctcttcaactg gctgggctgc tgcttctctc tgccttcttg 750
 gaggtgccct acttttgctgt tcctgtcccc gaaaaacaac ctcttaccca 800
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Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly
50 55 60
Gln Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser
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80 85 90
Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met
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Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val
110 115 120

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Phe Thr Gly Trp Ala Ala Ala Ser Leu	Cys Leu Leu Gly Gly Ala	
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<213> Homo sapiens

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 cnnngnnntct atgaccctat gacccagtc aatgccaggt acgaatttgg 450
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<210> 275
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 <222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274
 <223> unknown base

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<210> 277
 <211> 200
 <212> DNA
 <213> Homo sapiens

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 <222> 34, 87, 138, 147, 163, 165-166, 172
 <223> unknown base

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 gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

Figure 1 consists of 12 sub-graphs (a-l) showing the time course of various physiological parameters over a 10-minute period. The parameters are: (a) Heart rate (b/min), (b) Systolic blood pressure (mmHg), (c) Diastolic blood pressure (mmHg), (d) Mean arterial pressure (mmHg), (e) Stroke volume (L/min), (f) Cardiac output (L/min), (g) Systemic vascular resistance (dyne/cm²), (h) Pulmonary artery pressure (mmHg), (i) Pulmonary artery flow (L/min), (j) Pulmonary artery resistance (dyne/cm²), (k) Pulmonary artery pressure (mmHg), and (l) Pulmonary artery flow (L/min). Each graph shows data for three groups: Control (open circles), Hypertensive (filled circles), and Hypertensive + Nitroglycerin (open squares). The x-axis for all graphs is Time (min) from 0 to 10. The y-axis scales vary for each parameter. In general, the hypertensive group shows higher values for most parameters compared to the control group. The addition of nitroglycerin to the hypertensive group results in a decrease in most parameters, particularly in the later part of the 10-minute period.

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 281

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<400> 282

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<211> 2285

<212> DNA

<213> Homo sapiens

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<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

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<223> unknown base

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<210> 287

<211> 270

<212> DNA

<213> Homo sapiens

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<221> unsure

<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242

<223> unknown base

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 catatccatg ggattttaaat ttatcataac catgtgtaaa aagaaattaa 150
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 acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
 agttaaaaat gtatagtaac 270

<210> 288

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 35, 116, 129, 197, 278, 294, 297, 349, 351

<223> unknown base

<400> 288
 ggtggcccat tcccggccca ggctgctttc cggtnntcag ttctgtccaa 50
 gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100
 gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150
 actgattgac ccagcgcttt ggaaataaat ggcagtgcctt tgttcantta 200
 aagggaccaa gctaaatttg tatttggttca tgtagtgaag tcaaactgtt 250
 attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300
 tgtttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350
 ntgttggggtg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400
 ttggagagtc tggatcatgtg gaggtggg 428

<210> 289
 <211> 320
 <212> DNA
 <213> Homo sapiens

<400> 289
 tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50
 atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100
 tactcgtcat aagtgagagg cgtgtgttga ctgattgacc cagcgctttg 150
 gaaataaatg gcagtgcctt gttcacttaa agggaccaag ctaaatttgt 200
 attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250
 atttaactta tttaatgtat ttcatctcat gttttcttat tgtcacaaga 300
 gtacagttaa tgctgcgtgc 320

<210> 290
 <211> 609
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
 447, 481, 513, 532, 584, 598
 <223> unknown base

<400> 290
 aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50
 gaaacntgn gtaatgccac aatggcatat tgtaaattgc attttaaaca 100
 ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150
 cttcctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200

ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250
 cccaggctgc tttccgtgtc ttcagttctg tccaagccat cagctccttg 300
 ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350
 cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccagc 400
 gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450
 atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500
 atgcatattt aanttattta atgtatttca tntcatgttt tcttattgtc 550
 acaagggtag agttaatgct gcgtgctgct gaantctgtt gggagaantg 600
 gtattgctg 609

<210> 291
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 291
 ggcccttgagg gagctggagc ccagcatgct ggggagtgcg gtcagctcca 50
 cacagtagtc cccaagtggc ccaactcccgg cccaggctgc tttccgtgtc 100
 ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150
 aagcccaaag gaattgcaact gtggcagcat cagacgtact cgtcataagt 200
 gagaggcgtg tgttgactga ttgaccagc gctttggaaa taaatggcag 250
 tgctttgttc acttaaaggg accaagctaa atttgtattg gttcatgtag 300
 tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350
 atgtatttca tctcatgttt tcttattgtc acaagagtag agttaatgct 400
 gcgtgctgct gaactctgtt gggagaactg gtattgctgc tggagggctg 450
 tgggctcctc tgtctctgga gagtctgggc atgtggaggt ggg 493

<210> 292
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 292
 gcaccaccgt aggtacttgt gtgaggc 27

<210> 293
 <211> 23
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcgggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccggctca 50

ggctggctga gaggtccca gctgcagcgt ccccgcccg ctcctcggga 100

gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150

gtctcacttt gttgccagg ctggagttca gtgccatgat catggtttac 200

tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250

acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300

atttttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350

attttatgtg gcacttgaga aaggtaaccc ggattgtcag tgaaaggact 400

ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450

tacagtgtgt ggcacgaat gccagaaaga actcccaact ccagccttt 500

ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550

cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600

aaatatcacc acaaaggag tatctgttag gagaaagaga cagggtgatg 650

gcaccgacag caggttcagc atcttgga aaaggttctt aaccaatttc 700

cctttcagca cagctgtgaa gctttccacg ggctgtagt gcattctcat 750

ttcccctcag catgtttotaa ctgctgccca ctgtgttcat gatggaaagg 800

actatgtcaa agggagtaaa aagctaagg tagggttggt gaagatgagg 850

aataaaagtg gaggcaagaa acgtcgaggt tctaagagga gcaggagaga 900
agctagtggg ggtgaccaa gagaggttac cagagagcat ctgcaggaga 950
gagcgaaggg tgggagaaga agaaaaaat ctggccgggg tcagaggatt 1000
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aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950
atagagacag aaagttacaa cacagtttgt actactctga gatggatcca 2000
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cctagtttag aaatagggaa gctgagacat tttaagatct caagttttta 2250
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cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350
 atacattcta tgtatgaggt gctacatttt taggacaaaag aattctgtaa 2400
 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450
 tgaggactat aggggtgaatt ctctgattag taattttaga tatgtccttt 2500
 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296
 <211> 413
 <212> PRT
 <213> Homo sapiens

<400> 296
 Met Glu Asn Met Leu Leu Trp Leu Ile Phe Phe Thr Pro Gly Trp
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 Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His
 20 25 30
 Leu Arg Lys Val Pro Arg Ile Val Ser Glu Arg Thr Phe His Leu
 35 40 45
 Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr
 50 55 60
 Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu
 65 70 75
 Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn
 80 85 90
 Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu
 95 100 105
 Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg
 110 115 120
 Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp
 125 130 135
 Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu
 140 145 150
 Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu
 155 160 165
 Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly
 170 175 180
 Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser
 185 190 195
 Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala
 200 205 210

Ser	Gly	Gly	Asp	Gln	Arg	Glu	Gly	Thr	Arg	Glu	His	Leu	Gln	Glu
				215					220					225
Arg	Ala	Lys	Gly	Gly	Arg	Arg	Arg	Lys	Lys	Ser	Gly	Arg	Gly	Gln
				230					235					240
Arg	Ile	Ala	Glu	Gly	Arg	Pro	Ser	Phe	Gln	Trp	Thr	Arg	Val	Lys
				245					250					255
Asn	Thr	His	Ile	Pro	Lys	Gly	Trp	Ala	Arg	Gly	Gly	Met	Gly	Asp
				260					265					270
Ala	Thr	Leu	Asp	Tyr	Asp	Tyr	Ala	Leu	Leu	Glu	Leu	Lys	Arg	Ala
				275					280					285
His	Lys	Lys	Lys	Tyr	Met	Glu	Leu	Gly	Ile	Ser	Pro	Thr	Ile	Lys
				290					295					300
Lys	Met	Pro	Gly	Gly	Met	Ile	His	Phe	Ser	Gly	Phe	Asp	Asn	Asp
				305					310					315
Arg	Ala	Asp	Gln	Leu	Val	Tyr	Arg	Phe	Cys	Ser	Val	Ser	Asp	Glu
				320					325					330
Ser	Asn	Asp	Leu	Leu	Tyr	Gln	Tyr	Cys	Asp	Ala	Glu	Ser	Gly	Ser
				335					340					345
Thr	Gly	Ser	Gly	Val	Tyr	Leu	Arg	Leu	Lys	Asp	Pro	Asp	Lys	Lys
				350					355					360
Asn	Trp	Lys	Arg	Lys	Ile	Ile	Ala	Val	Tyr	Ser	Gly	His	Gln	Trp
				365					370					375
Val	Asp	Val	His	Gly	Val	Gln	Lys	Asp	Tyr	Asn	Val	Ala	Val	Arg
				380					385					390
Ile	Thr	Pro	Leu	Lys	Tyr	Ala	Gln	Ile	Cys	Leu	Trp	Ile	His	Gly
				395					400					405
Asn	Asp	Ala	Asn	Cys	Ala	Tyr	Gly							
				410										

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcatctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 298
catcgttccc gtgaatccag aggc 24

<210> 299
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 299
gaaggaggc cttcctttca gtggacccgg gtcaagaata cccac 45

<210> 300
<211> 1869
<212> DNA
<213> Homo sapiens

<400> 300
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ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150
gcaactcctg gcacactgct cctctttctg gctttcctgc tcctgagttc 200
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taagtgaat catctacca aagctttttg gctctcaaat taaagattga 1850
ttagtttcaa aaaaaaaaaa 1869

<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe
1 5 10 15

Leu Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu
20 25 30

Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys
35 40 45

Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys
50 55 60

Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr	
				65					70					75	
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala	
				80					85					90	
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe	
				95					100					105	
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser	
				110					115					120	
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala	
				125					130					135	
Pro	Lys	Val	Leu	Asp	Gly	Thr	Arg	Cys	Tyr	Thr	Glu	Ser	Leu	Asp	
				140					145					150	
Met	Cys	Ile	Ser	Gly	Leu	Cys	Gln	Ile	Val	Gly	Cys	Asp	His	Gln	
				155					160					165	
Leu	Gly	Ser	Thr	Val	Lys	Glu	Asp	Asn	Cys	Gly	Val	Cys	Asn	Gly	
				170					175					180	
Asp	Gly	Ser	Thr	Cys	Arg	Leu	Val	Arg	Gly	Gln	Tyr	Lys	Ser	Gln	
				185					190					195	
Leu	Ser	Ala	Thr	Lys	Ser	Asp	Asp	Thr	Val	Val	Ala	Leu	Pro	Tyr	
				200					205					210	
Gly	Ser	Arg	His	Ile	Arg	Leu	Val	Leu	Lys	Gly	Pro	Asp	His	Leu	
				215					220					225	
Tyr	Leu	Glu	Thr	Lys	Thr	Leu	Gln	Gly	Thr	Lys	Gly	Glu	Asn	Ser	
				230					235					240	
Leu	Ser	Ser	Thr	Gly	Thr	Phe	Leu	Val	Asp	Asn	Ser	Ser	Val	Asp	
				245					250					255	
Phe	Gln	Lys	Phe	Pro	Asp	Lys	Glu	Ile	Leu	Arg	Met	Ala	Gly	Pro	
				260					265					270	
Leu	Thr	Ala	Asp	Phe	Ile	Val	Lys	Ile	Arg	Asn	Ser	Gly	Ser	Ala	
				275					280					285	
Asp	Ser	Thr	Val	Gln	Phe	Ile	Phe	Tyr	Gln	Pro	Ile	Ile	His	Arg	
				290					295					300	
Trp	Arg	Glu	Thr	Asp	Phe	Phe	Pro	Cys	Ser	Ala	Thr	Cys	Gly	Gly	
				305					310					315	
Gly	Tyr	Gln	Leu	Thr	Ser	Ala	Glu	Cys	Tyr	Asp	Leu	Arg	Ser	Asn	
				320					325					330	
Arg	Val	Val	Ala	Asp	Gln	Tyr	Cys	His	Tyr	Tyr	Pro	Glu	Asn	Ile	
				335					340					345	
Lys	Pro	Lys	Pro	Lys	Leu	Gln	Glu	Cys	Asn	Leu	Asp	Pro	Cys	Pro	

350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His		
365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser		
380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu		
395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys		
410	415	420
Met Tyr Thr Pro Lys Met Pro Ile Ala Gln Pro Cys Asn Ile Phe		
425	430	435
Asp Cys Pro Lys Trp Leu Ala Gln Glu Trp Ser Pro Cys Thr Val		
440	445	450
Thr Cys Gly Gln Gly Leu Arg Tyr Arg Val Val Leu Cys Ile Asp		
455	460	465
His Arg Gly Met His Thr Gly Gly Cys Ser Pro Lys Thr Lys Pro		
470	475	480
His Ile Lys Glu Glu Cys Ile Val Pro Thr Pro Cys Tyr Lys Pro		
485	490	495
Lys Glu Lys Leu Pro Val Glu Ala Lys Leu Pro Trp Phe Lys Gln		
500	505	510
Ala Gln Glu Leu Glu Glu Gly Ala Ala Val Ser Glu Glu Pro Ser		
515	520	525

<210> 302
 <211> 1533
 <212> DNA
 <213> Homo sapiens

<400> 302
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 ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100
 ctgggcgggg cgctgtggct ggcggcccgc cgttcgtgg ggcccagggt 150
 ccagcggctg cgcagaggcg gggaccccg cctcatgcac gggaagactg 200
 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgccgag 250
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300
 cgccgaggag gcggcggtc agctccgccg cgagctccgc caggccgcgg 350
 agtgcggccc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400
 gagctggacc tcgcctcgct gcgctcgggt gcgccttct gccaggaaat 450

gctccaggaa gaggcctaggc tggatgtctt gatcaataac gcagggatct 500
tccagtgtccc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550
gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600
caaaagttca gctcccagca ggattgtggt agtttcttcc aaactttata 650
aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700
aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750
ggaactagcc cgccgcttag aaggcacaaa tgtcaccgtc aatgtgttgc 800
atcctggtat tgtacggaca aatctgggga ggcacataca cattccactg 850
ttggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaaactcc 900
agtagaaggt gcccgactt ccattttattt ggcctcttca cctgaggtag 950
aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000
cccaaagcta tggatgaatc tggtgcaaga aaactctggg atatcagtga 1050
agtgatggtt ggcttgctaa aataggaaca aggagtaaaa gagctgttta 1100
taaaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150
acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200
ggtacatgtg ggtattttgg agttactgaa aaattatttt tgggataaga 1250
gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300
aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350
tggatgacat attaatatit gtcagaatta agtgactcaa agtgctatcg 1400
agagggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
ttactacaat gtttggtggt tgtgtggaaa ttatctgcct ggtgtgtgca 1500
cacaagtctt acttgaata aatttactgg tac 1533

<210> 303
<211> 336
<212> PRT
<213> Homo sapiens

<400> 303
Met Ala Val Ala Thr Ala Ala Ala Val Leu Ala Ala Leu Gly Gly
1 5 10 15
Ala Leu Trp Leu Ala Ala Arg Arg Phe Val Gly Pro Arg Val Gln
20 25 30
Arg Leu Arg Arg Gly Gly Asp Pro Gly Leu Met His Gly Lys Thr
35 40 45

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala	
				50					55					60	
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg	
				65					70					75	
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu	
				80					85					90	
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly	
				95					100					105	
Val	Gly	Glu	Leu	Ile	Val	Arg	Glu	Leu	Asp	Leu	Ala	Ser	Leu	Arg	
				110					115					120	
Ser	Val	Arg	Ala	Phe	Cys	Gln	Glu	Met	Leu	Gln	Glu	Glu	Pro	Arg	
				125					130					135	
Leu	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Phe	Gln	Cys	Pro	Tyr	
				140					145					150	
Met	Lys	Thr	Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	
				155					160					165	
Leu	Gly	His	Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Gly	Leu	Leu	Lys	
				170					175					180	
Ser	Ser	Ala	Pro	Ser	Arg	Ile	Val	Val	Val	Ser	Ser	Lys	Leu	Tyr	
				185					190					195	
Lys	Tyr	Gly	Asp	Ile	Asn	Phe	Asp	Asp	Leu	Asn	Ser	Glu	Gln	Ser	
				200					205					210	
Tyr	Asn	Lys	Ser	Phe	Cys	Tyr	Ser	Arg	Ser	Lys	Leu	Ala	Asn	Ile	
				215					220					225	
Leu	Phe	Thr	Arg	Glu	Leu	Ala	Arg	Arg	Leu	Glu	Gly	Thr	Asn	Val	
				230					235					240	
Thr	Val	Asn	Val	Leu	His	Pro	Gly	Ile	Val	Arg	Thr	Asn	Leu	Gly	
				245					250					255	
Arg	His	Ile	His	Ile	Pro	Leu	Leu	Val	Lys	Pro	Leu	Phe	Asn	Leu	
				260					265					270	
Val	Ser	Trp	Ala	Phe	Phe	Lys	Thr	Pro	Val	Glu	Gly	Ala	Gln	Thr	
				275					280					285	
Ser	Ile	Tyr	Leu	Ala	Ser	Ser	Pro	Glu	Val	Glu	Gly	Val	Ser	Gly	
				290					295					300	
Arg	Tyr	Phe	Gly	Asp	Cys	Lys	Glu	Glu	Glu	Leu	Leu	Pro	Lys	Ala	
				305					310					315	
Met	Asp	Glu	Ser	Val	Ala	Arg	Lys	Leu	Trp	Asp	Ile	Ser	Glu	Val	
				320					325					330	
Met	Val	Gly	Leu	Leu	Lys										

<210> 304
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 20, 34, 62, 87, 221, 229
 <223> unknown base

<400> 304
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 gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100
 ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150
 gtgatcagga atgggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
 tttgatattg gaatagcctg ntaagaggna catgtgggta ttttgagatt 250
 actgaaaaat tatttttggg ataagagaat ttcagcaaag atgttttaaa 300
 tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
 attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
 gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
 tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500
 tggaaattat ctgcctggct t 521

<210> 305
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 305
 ccaggaaatg ctccaggaag agcc 24

<210> 306
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 306
 gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307
aacgcaggga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308
<211> 1523
<212> DNA
<213> Homo sapiens

<400> 308
gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50
cggagcccag ccctttccta acccaaccca acctagccca gtcccagccg 100
ccagcgcttg tccctgtcac ggaccccgagc gttaccatgc atcctgccgt 150
cttcctatcc ttacccgacc tcagatgctc ctttctgctc ctggtaactt 200
gggtttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250
atagatgaaa ttttaaacaa tgctgatgtt gctttagtaa atttttatgc 300
tgactggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650
cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850
gataaatgtg ttcctcttgt ccgagaaata acatttgaaa atggagagga 900
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000
agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050

acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100
 ctattgacag ctttaggcatt atgtatgtgt ttggagactt caaagatgta 1150
 ttaattcctg gaaaactcaa gcaattcgta ttgacttac attctggaaa 1200
 actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250
 gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300
 aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350
 gcttttaaaaa cttgaaaaac agtttgtaag cttttcaaca gcagcatcaa 1400
 cctacgtggg ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450
 tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309
 <211> 406
 <212> PRT
 <213> Homo sapiens

<400> 309
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 1 5 10 15
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 20 25 30
 Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn
 35 40 45
 Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe
 50 55 60
 Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile
 65 70 75
 Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val
 80 85 90
 Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser
 95 100 105
 Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys
 110 115 120
 Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr
 125 130 135
 Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu
 140 145 150
 Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly
 155 160 165

Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg	170	175	180
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe	185	190	195
Gly	Asp	Val	Ser	Lys	Pro	Glu	Arg	Tyr	Ser	Gly	Asp	Asn	Ile	Ile	200	205	210
Tyr	Lys	Pro	Pro	Gly	His	Ser	Ala	Pro	Asp	Met	Val	Tyr	Leu	Gly	215	220	225
Ala	Met	Thr	Asn	Phe	Asp	Val	Thr	Tyr	Asn	Trp	Ile	Gln	Asp	Lys	230	235	240
Cys	Val	Pro	Leu	Val	Arg	Glu	Ile	Thr	Phe	Glu	Asn	Gly	Glu	Glu	245	250	255
Leu	Thr	Glu	Glu	Gly	Leu	Pro	Phe	Leu	Ile	Leu	Phe	His	Met	Lys	260	265	270
Glu	Asp	Thr	Glu	Ser	Leu	Glu	Ile	Phe	Gln	Asn	Glu	Val	Ala	Arg	275	280	285
Gln	Leu	Ile	Ser	Glu	Lys	Gly	Thr	Ile	Asn	Phe	Leu	His	Ala	Asp	290	295	300
Cys	Asp	Lys	Phe	Arg	His	Pro	Leu	Leu	His	Ile	Gln	Lys	Thr	Pro	305	310	315
Ala	Asp	Cys	Pro	Val	Ile	Ala	Ile	Asp	Ser	Phe	Arg	His	Met	Tyr	320	325	330
Val	Phe	Gly	Asp	Phe	Lys	Asp	Val	Leu	Ile	Pro	Gly	Lys	Leu	Lys	335	340	345
Gln	Phe	Val	Phe	Asp	Leu	His	Ser	Gly	Lys	Leu	His	Arg	Glu	Phe	350	355	360
His	His	Gly	Pro	Asp	Pro	Thr	Asp	Thr	Ala	Pro	Gly	Glu	Gln	Ala	365	370	375
Gln	Asp	Val	Ala	Ser	Ser	Pro	Pro	Glu	Ser	Ser	Phe	Gln	Lys	Leu	380	385	390
Ala	Pro	Ser	Glu	Tyr	Arg	Tyr	Thr	Leu	Leu	Arg	Asp	Arg	Asp	Glu	395	400	405

Leu

<210> 310
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure

<222> 36, 48
<223> unknown base

<400> 310
attaaggaag aatttcctaaa tgaaaatcaa gtagtntttg ccagagtnga 50
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396
<223> unknown base

<400> 311
agaggcctct ctggaagttg tcccgggtgt tcgccgcngg agcccgggtc 50
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100
cggagcccag ccctttccta acccaaccca acctagcccn gtcccagccg 150
ccagcgcctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200
cttcctatcc ttaccogacc tcagatgctc ccttctgctc ctggttaactt 250
gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300
atagatgaaa ttttaaacna tgctgatgtg gcttttagtca atttttatgc 350
tgactgggtg cgtttcagtc agatgtggca tccaattttt gaggangctt 400
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450
agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 500
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 312
tgagaggcct ctctggaagt tg 22

<210> 313
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 313
 gtcagcgatc agtgaaagc 19

 <210> 314
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 314
 ccagaatgaa gtagctcggc 20

 <210> 315
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 315
 ccgactcaaa atgcattgtc 20

 <210> 316
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 316
 catttggcag gaattgtcc 19

 <210> 317
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 317
 ggtgctatag gccaaggg 18

 <210> 318
 <211> 24
 <212> DNA

Figure 1. Schematic representation of the experimental design. The figure is divided into two main sections: 'Pre-Test' and 'Main Test'. The 'Pre-Test' section includes 'Pre-Test 1' and 'Pre-Test 2', both of which involve 'Pre-Test 1' and 'Pre-Test 2' phases. The 'Main Test' section includes 'Main Test 1' and 'Main Test 2', both of which involve 'Main Test 1' and 'Main Test 2' phases. The 'Pre-Test' section also includes 'Pre-Test 1' and 'Pre-Test 2' phases. The 'Main Test' section also includes 'Main Test 1' and 'Main Test 2' phases. The 'Pre-Test' section also includes 'Pre-Test 1' and 'Pre-Test 2' phases. The 'Main Test' section also includes 'Main Test 1' and 'Main Test 2' phases.

tgatcagtta ctttaaaaaa tgactcctta ttttttaa at gtttccacat 600
 ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650
 taaatggtat tacgtataaa ttaatatata atgattacct ctggtgttga 700
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800
 cttgtagggc tcatttttgg ttcattgaaa cagtatctaa ttataaatta 850
 gctgtagata tcaggtgctt ctgatgaagt gaaaatgtat atctgactag 900
 tgggaaactt catgggtttc ctcactgtgc atgtcgatga ttatatatgg 950
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000
 tcctgtgata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050
 taaatatact tgctttaatt cttaagcata agtaaacaatg atataaaaat 1100
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaatgtgt 1150
 tttttattgt aagacattac ttattaagaa attggttatt atgcttactg 1200
 ttctaactctg gtggttaaagg tattcttaag aatttgcagg tactacagat 1250
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 322
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu
 1 5 10 15
 Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala
 20 25 30
 Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys
 35 40 45
 Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala
 50 55 60
 Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu
 65 70 75
 Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met
 80 85 90
 Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr
 95 100 105

Ile	Met	Asn	Ala	Asp	Ile	Leu	Ala	Tyr	Cys	Gln	Lys	Glu	Gly	Trp
				110					115					120
Cys	Lys	Leu	Ala	Phe	Tyr	Leu	Leu	Ala	Phe	Phe	Tyr	Tyr	Leu	Tyr
				125					130					135
Gly	Met	Ile	Tyr	Val	Leu	Val	Ser	Ser						
				140										

<210> 323
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 323
 attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50
 tgtaataccc tgaatcccct tgtactccca gactacctca tccacgcttt 100
 cttctgtgtc atgtttcttt gtgcagcaga gtgggttaca ctgggtctca 150
 atatgcccct cttggcatat catatttggg ggtatatgag tagaccagtg 200
 atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250
 tctagcatat tgtcagaagg aaggatgggtg caaattagct ttttatcttc 300
 tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350
 tagaacaaca cacagaagaa ttggtccagt taagtgcag caaaaagcca 400
 ccaaatagaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450
 gaatctgatc agttacttta aaaaatg 477

<210> 324
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 324
 tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 325
 caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaccaa ttcttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tggtagcaat tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
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ggacccaact ggggctcccg ccgctgctgc tgctgaccat ggccttggcc 150
ggagggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250
accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300
tcaatttgtc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450
caagaacaac ttatgtcoct gatgccaaaa atgcacctac tctttcctct 500

aactctggtg aggtcattct ggagtgacat gatggactcc gcacagagct 550
tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600
gttatattcc agtctaagcc agaaatccag tacgcaccac atttgagca 650
ggagcctaca aatttgagag aatcatctct aagcaaatg tcctatctgc 700
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gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800
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ttttaaaaga caagtgaat agacatctaa aattccactc ctcatagagc 1100
ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150
caaataaagt tactcaaatc tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

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Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
			20						25					30
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35						40					45
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
			50						55					60
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65						70					75
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80						85					90
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95						100					105
Gln	Ser	Asp	Glu	Gln	Tyr	Ala	Cys	His	Leu	Gly	Cys	Gln	Asn	Gln
			110						115					120

Leu	Pro	Phe	Ala	Glu	Leu	Arg	Gln	Glu	Gln	Leu	Met	Ser	Leu	Met	
				125					130					135	
Pro	Lys	Met	His	Leu	Leu	Phe	Pro	Leu	Thr	Leu	Val	Arg	Ser	Phe	
				140					145					150	
Trp	Ser	Asp	Met	Met	Asp	Ser	Ala	Gln	Ser	Phe	Ile	Thr	Ser	Ser	
				155					160					165	
Trp	Thr	Phe	Tyr	Leu	Gln	Ala	Asp	Asp	Gly	Lys	Ile	Val	Ile	Phe	
				170					175					180	
Gln	Ser	Lys	Pro	Glu	Ile	Gln	Tyr	Ala	Pro	His	Leu	Glu	Gln	Glu	
				185					190					195	
Pro	Thr	Asn	Leu	Arg	Glu	Ser	Ser	Leu	Ser	Lys	Met	Ser	Tyr	Leu	
				200					205					210	
Gln	Met	Arg	Asn	Ser	Gln	Ala	His	Arg	Asn	Phe	Leu	Glu	Asp	Gly	
				215					220					225	
Glu	Ser	Asp	Gly	Phe	Leu	Arg	Cys	Leu	Ser	Leu	Asn	Ser	Gly	Trp	
				230					235					240	
Ile	Leu	Thr	Thr	Thr	Leu	Val	Leu	Ser	Val	Met	Val	Leu	Leu	Trp	
				245					250					255	
Ile	Cys	Cys	Ala	Thr	Val	Ala	Thr	Ala	Val	Glu	Gln	Tyr	Val	Pro	
				260					265					270	
Ser	Glu	Lys	Leu	Ser	Ile	Tyr	Gly	Asp	Leu	Glu	Phe	Met	Asn	Glu	
				275					280					285	
Gln	Lys	Leu	Asn	Arg	Tyr	Pro	Ala	Ser	Ser	Leu	Val	Val	Val	Arg	
				290					295					300	
Ser	Lys	Thr	Glu	Asp	His	Glu	Glu	Ala	Gly	Pro	Leu	Pro	Thr	Lys	
				305					310					315	
Val	Asn	Leu	Ala	His	Ser	Glu	Ile								
				320											

<210> 331

<211> 350

<212> DNA

<213> Homo sapiens

<400> 331

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gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 100
ggctgttttc aatttgctcag tttgtggatg atggaattga cttaaattcga 150
actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaattctga 200
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgtctg 250

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aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300
tttctcttaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332
<211> 562
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 47
<223> unknown base

<400> 332
cacactggcc ggatctttta gagtcctttg accttgacca agggtcngga 50
aaacagcaac aagctgagct gctgtgacag agggacaag atggcggcgc 100
cgaagggagc ctttggtgga ggaccaact ggggtccccg ccgctgctgc 150
tgctgaccat ggcttgggcc ggaggttcgg ggaccgcttc ggctgaagca 200
tttgactcgg tcttggtgga tacggcgtct tgccaccggg cctgtcagtt 250
gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300
agagagggtg caggctgttt tcaatttgct agtttgtgga tgatggaatt 350
gacttaaata gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400
ttccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450
tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgcaaaa 500
atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550
gatggactcc gc 562

<210> 333
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 333
acaagctgag ctgctgtgac ag 22

<210> 334
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 334
tgattctggc aaccaagatg gc 22

<210> 335
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 335
atggccttgg ccggagggtc ggggaccgct tcggctgaag 40

<210> 336
<211> 1885
<212> DNA
<213> Homo sapiens

<400> 336
gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50
cgggccggag gtggggcgcc gctggggccg gcccgcacgg gcttcatctg 100
agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150
gcgacaagct gccggagctg caatgggccg cggctgggga ttcttgtttg 200
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250
cccccggaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300
ggatgattgt acctgtgatg ttgaaacat tgatagattt aataactaca 350
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600
tctgagttag gaaacacaga aggtgttct tcagtggacc aagcatgatg 650
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750
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agccacagac aattaaaaga ctttaaatc ctttggcttc tggatcaagg 850
acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900
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 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgcccagat 1150
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatggt 1200
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 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450
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 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaaact 1550
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 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337
 <211> 468
 <212> PRT
 <213> Homo sapiens

<400> 337
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 Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr
 20 25 30
 Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp
 35 40 45
 Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg
 50 55 60
 Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg
 65 70 75

Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp	
				80					85					90	
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln	
				95					100					105	
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr	
				110					115					120	
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu	
				125					130					135	
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys	
				140					145					150	
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe	
				155					160					165	
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp	
				170					175					180	
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp	
				185					190					195	
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys	
				200					205					210	
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln	
				215					220					225	
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu	
				230					235					240	
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His	
				245					250					255	
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu	
				260					265					270	
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln	
				275					280					285	
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg	
				290					295					300	
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu	
				305					310					315	
Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	
				320					325					330	
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	
				335					340					345	
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	
				350					355					360	
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys	

	365		370		375
Glu Asp Phe Arg	Leu His Phe Arg Asn	Ile Ser Arg Ile Met Asp			
	380	385		390	
Cys Val Gly Cys	Phe Lys Cys Arg Leu	Trp Gly Lys Leu Gln Thr			
	395	400		405	
Gln Gly Leu Gly	Thr Ala Leu Lys Ile	Leu Phe Ser Glu Lys Leu			
	410	415		420	
Ile Ala Asn Met	Pro Glu Ser Gly Pro	Ser Tyr Glu Phe His Leu			
	425	430		435	
Thr Arg Gln Glu	Ile Val Ser Leu Phe	Asn Ala Phe Gly Arg Ile			
	440	445		450	
Ser Thr Ser Val	Lys Glu Leu Glu Asn	Phe Arg Asn Leu Leu Gln			
	455	460		465	
Asn Ile His					

<210> 338
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 101, 263, 376, 397, 426
 <223> unknown base

<400> 338
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 ttaaaagacc tttaaactct ttggcttctg gtcaagggac aagtgaagag 100
 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200
 caagatatct tttaacaagag acctgggttag aaaagaaatg gggacacaac 250
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350
 ctttatccaa agtgttacca ttcttngagc gccagattt tcaactnttt 400
 actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450
 acttcatgaa atcaagtcatt ttcctttgca ttttgatgag aattcatttt 500
 tttgctg 507

<210> 339
 <211> 20

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 339
aagctgccgg agctgcaatg 20

<210> 340
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 340
ttgcttctta atcctgagcg c 21

<210> 341
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 341
aaaggaggac tttcgactgc 20

<210> 342
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 342
agagattcat ccactgctcc aagtcg 26

<210> 343
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 343
tgtccagaaa caggcacata tcagc 25

<210> 344
<211> 50
<212> DNA
<213> Artificial Sequence

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<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tgggcggacg cgtgggttgg gagggggcag 50
gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100
ggactttctca tactggacag aaaccgatca ggcatggaac tccccttcgt 150
caotcaoctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200
ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250
gaatttgat acagtgtctt acaacatgtt gggggtggac agcgatgat 300
gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350
tttatcgctg ccctgtaggg ggggccaca atgccccatg tgccaagggc 400
cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450
gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500
tgagctaagg agaggggtgg ggcagtgtct ctgaagggtcc ataaaagaaa 550
aaagagaagt gtggttaagg aaaatggtct gtgtggaggg gtcaaggagt 600
taaaaacct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650
gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700
gtaactatct ccccatccc caggcctgtg cccctctctg gtctcgtgct 750
tgtggcagct ctgtcttcag ttctgggata tgtgcccgtg tggatgcttc 800
attccagcct cagggaagcc tggcaccac tgcccaacgt gagccagagg 850
aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900
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gctacctaata gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000
cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050
caagggtggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100
catggtgaaa ctccatctct actaaaaaaaa aaaaaatata aaaattagct 1150

ggggtgcgcta gtgcatgcct gtaatctcat ctactcggga ggctaagaca 1200
 ggagactctc acttcaaccc aggaggtgga gggtgcggtg agccaagatt 1250
 gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300
 aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350
 gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
 gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450
 agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 346
 Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe
 1 5 10 15
 Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro
 20 25 30
 Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val
 35 40 45
 Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala
 50 55 60
 Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg
 65 70 75
 Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His
 80 85 90
 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn
 95 100 105
 Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly
 110 115 120
 Phe Met Val Ser

<210> 347
 <211> 509
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 22
 <223> unknown base

<400> 347

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 ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
 ggagagggac agaggccaga ggacttctca tactggacag aaaccgatca 150
 ggcattggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttct 200
 gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250
 tcccagggcc accagaagct gaatttggat acagtgtctt acaacatggt 300
 gggggtggac agcgatggat gctggtgggc gccccctggg atgggccttc 350
 aggcgaccgg aggggggacg tttatcgctg ccctgtaggg ggggcccaca 400
 atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
 tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500
 tggatgatgg 509

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 348
 agggacagag gccagaggac ttc 23

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 349
 caggtgcata ttcacagcag gatg 24

<210> 350
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 350
 ggaactcccc ttcgtcactc acctgttctt gccccctggg ttcct 45

<210> 351
 <211> 2056
 <212> DNA

<213> Homo sapiens

<400> 351

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catctgggtt tgggcagaaa ggaggggtgct tcggagcccg ccctttctga 100
gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200
gctttatttt ggaaagaaac aatgttctag gtcaaactga gtctacaaa 250
tgcagacttt cacaatggtt ctagaagaaa tctggacaag tcttttcatg 300
tggtttttct acgcattgat tccatgtttg ctacacagatg aagtggccat 350
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400
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 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950
 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000
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 aaaaaa 2056

<210> 352

<211> 311

<212> PRT

<213> Homo sapiens

<400> 352

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu
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Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
			20						25					30
Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser
			35						40					45
Thr	Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro
			50						55					60
Gly	Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu
			65						70					75
Ser	Leu	Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser
			80						85					90
Leu	Thr	Glu	Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala
			95						100					105
Thr	Val	Pro	Tyr	Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln
			110						115					120

Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	
				125					130					135	
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	
				140					145					150	
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	
				155					160					165	
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val	
				170					175					180	
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met	
				185					190					195	
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys	
				200					205					210	
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu	
				215					220					225	
Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe	
				230					235					240	
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp	
				245					250					255	
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val	
				260					265					270	
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile	
				275					280					285	
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met	
				290					295					300	
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser					
				305					310						

<210> 353

<211> 864

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 654, 711, 748, 827

<223> unknown base

<400> 353

tcctgctgat gcacatctgg gtttggcaaa aggagggttc ttcgagccgc 50

cctttctagc ttctggccg gctctagaac aattcaggct tcgctgac 100

tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150

agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200

ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250
 tcatgtggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300
 gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400
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 gaaccoccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800
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 ggcgctgggt tgat 864

<210> 354
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 354
 aggccttcgct gcgactagac ctc 23

 <210> 355
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 355
 ccaggtcggg taaggatggt tgag 24

 <210> 356
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

<400> 356
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357
<211> 1670
<212> DNA

<213> Homo sapiens

<400> 357
cccacgcgtc cgcccacgcg tccgaggagc aagagagaag agagactgaa 50
acaggagagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100
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agaggcagga gctggaaagg agagaggagag gaggaggagg agatgcggga 200
tgagagacctg gagttagggt gcttgggaga gcttaatgaa aagagaacgg 250
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ggaaaagagc agaggaaaga ggaaagacac agagagacgg gagagagaag 400
aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450
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ggacagggtc ccagaaggag gggacagagg agctgagaga ggggggcagg 550
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<210> 358
<211> 328
<212> PRT
<213> Homo sapiens

<400> 358
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Trp Ala Ala Leu Gly Ala Ala Ala His Ile Gly Pro Ala Pro Asp
20 25 30
Pro Glu Asp Trp Trp Ser Tyr Lys Asp Asn Leu Gln Gly Asn Phe
35 40 45
Val Pro Gly Pro Pro Phe Trp Gly Leu Val Asn Ala Ala Trp Ser
50 55 60
Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu
65 70 75
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser
80 85 90
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg
95 100 105
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser
110 115 120
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu
125 130 135
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn
140 145 150
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln
155 160 165
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly

	170		175		180
Leu Ala Ile Leu	Ser Leu Phe Val Asn	Val Ala Ser Thr Ser	Asn		
	185		190		195
Pro Phe Leu Ser	Arg Leu Leu Asn Arg	Asp Thr Ile Thr Arg	Ile		
	200		205		210
Ser Tyr Lys Asn	Asp Ala Tyr Phe Leu	Gln Asp Leu Ser Leu	Glu		
	215		220		225
Leu Leu Phe Pro	Glu Ser Phe Gly Phe	Ile Thr Tyr Gln Gly	Ser		
	230		235		240
Leu Ser Thr Pro	Pro Cys Ser Glu Thr	Val Thr Trp Ile Leu	Ile		
	245		250		255
Asp Arg Ala Leu	Asn Ile Thr Ser Leu	Gln Met His Ser Leu	Arg		
	260		265		270
Leu Leu Ser Gln	Asn Pro Pro Ser Gln	Ile Phe Gln Ser Leu	Ser		
	275		280		285
Gly Asn Ser Arg	Pro Leu Gln Pro Leu	Ala His Arg Ala Leu	Arg		
	290		295		300
Gly Asn Arg Asp	Pro Arg His Pro Glu	Arg Arg Cys Arg Gly	Pro		
	305		310		315
Asn Tyr Arg Leu	His Val Asp Gly Val	Pro His Gly Arg			
	320		325		

<210> 359

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

tctgctgagg tgcagctcat tcac 24

<210> 360

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

gaggctctgg aagatctgag atgg 24

<210> 361

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 361

gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362

<211> 3038

<212> DNA

<213> Homo sapiens

<400> 362

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ccgccagcct ccgccgccga gcctcgttcg tgtccccgcc cctcgctcct 100

gcagctactg ctcagaaacg ctggggcgcc caccctggca gactaacgaa 150

gcagctccct tcccacocca actgcaggtc taattttgga cgctttgcct 200

gccatttctt ccaggttgag ggagccgcag aggcggaggc tcgcgtattc 250

ctgcagtcag caccacogtc gcccccgac gctcggtgct caggcccttc 300

gcgagcgggg ctctccgtct gcggctccct gtgaaggctc tgggcggctg 350

cagaggccgg ccgtccggtt tggctcacct ctcccaggaa acttcacact 400

ggagagccaa aaggagtgga agagcctgtc ttggagattt tcctggggaa 450

atcctgaggt cattcattat gaagtgtacc gcgcgggagt ggctcagagt 500

aaccacagtg ctgttcatgg ctagagcaat tccagccatg gtggttccca 550

atgccacttt attggagaaa cttttggaaa aatacatgga tgaggatggt 600

gagtggtgga tagccaaaca acgagggaaa agggccatca cagacaatga 650

catgcagagt attttggacc ttcataataa attacgaagt cagggtgtatc 700

caacagcctc taatatggag tatatgacat gggatgtaga gctggaaaga 750

tctgcagaat cctgggctga aagttgcttg tgggaacatg gacctgcaag 800

cttgcttcca tcaattggac agaatttggg agcacactgg ggaagatata 850

ggcccccgac gtttcatgta caatcgtggt atgatgaagt gaaagacttt 900

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tggccctgta tgtacacatt atacacaggc cgtgtgggca actagtaaca 1000

gaatcggttg tgccattaat ttgtgtcata acatgaacat ctgggggcag 1050

atatggcca aagctgtcta cctggtgtgc aattactccc caaagggaaa 1100

ctggtggggc catgcccctt acaaacatgg gcggccctgt tctgcttgcc 1150

cacctagttt tggagggggc tgtagagaaa atctgtgcta caaagaagg 1200
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acagcagtca caagtccatg acacccatgt cgggacaaga tcagatgata 1300
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tgatgtaatg cctgtggaca aaagaaagac ctacattgct tcttttcaga 1900
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actattccaa atgcaatatt tctgaatttt gtataaaact gtaacattac 2050
tgtacagagt acatcaacta ttttcagccc aaaaagggtgc caaatgcata 2100
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gctatatttt cttagcagtt atttctacag ttaattacat agtcatgatt 2250
gttctacgtt tcatatatta tatggtgctt tgtatatgcc actaataaaa 2300
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aaattctgat attgcacttc ttattttata taaaataatc ctttaatatc 2550
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[illegible]

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr
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Leu Leu Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu
35 40 45

Trp Trp Ile Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn
50 55 60

Asp Met Gln Ser Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln
65 70 75

Val Tyr Pro Thr Ala Ser Asn Met Glu Tyr Met Thr Trp Asp Val
80 85 90

Glu Leu Glu Arg Ser Ala Glu Ser Trp Ala Glu Ser Cys Leu Trp
95 100 105

Glu His Gly Pro Ala Ser Leu Leu Pro Ser Ile Gly Gln Asn Leu
110 115 120

Gly Ala His Trp Gly Arg Tyr Arg Pro Pro Thr Phe His Val Gln
125 130 135

Ser Trp Tyr Asp Glu Val Lys Asp Phe Ser Tyr Pro Tyr Glu His
140 145 150

Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys Ser Gly Pro Val Cys
155 160 165

Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser Asn Arg Ile Gly

	170		175		180
Cys Ala Ile Asn	Leu Cys His Asn Met	Asn Ile Trp Gly Gln Ile			
	185	190			195
Trp Pro Lys Ala	Val Tyr Leu Val Cys	Asn Tyr Ser Pro Lys Gly			
	200	205			210
Asn Trp Trp Gly	His Ala Pro Tyr Lys	His Gly Arg Pro Cys Ser			
	215	220			225
Ala Cys Pro Pro	Ser Phe Gly Gly Gly	Cys Arg Glu Asn Leu Cys			
	230	235			240
Tyr Lys Glu Gly	Ser Asp Arg Tyr Tyr	Pro Pro Arg Glu Glu Glu			
	245	250			255
Thr Asn Glu Ile	Glu Arg Gln Gln Ser	Gln Val His Asp Thr His			
	260	265			270
Val Arg Thr Arg	Ser Asp Asp Ser Ser	Arg Asn Glu Val Ile Ser			
	275	280			285
Ala Gln Gln Met	Ser Gln Ile Val Ser	Cys Glu Val Arg Leu Arg			
	290	295			300
Asp Gln Cys Lys	Gly Thr Thr Cys Asn	Arg Tyr Glu Cys Pro Ala			
	305	310			315
Gly Cys Leu Asp	Ser Lys Ala Lys Val	Ile Gly Ser Val His Tyr			
	320	325			330
Glu Met Gln Ser	Ser Ile Cys Arg Ala	Ala Ile His Tyr Gly Ile			
	335	340			345
Ile Asp Asn Asp	Gly Gly Trp Val Asp	Ile Thr Arg Gln Gly Arg			
	350	355			360
Lys His Tyr Phe	Ile Lys Ser Asn Arg	Asn Gly Ile Gln Thr Ile			
	365	370			375
Gly Lys Tyr Gln	Ser Ala Asn Ser Phe	Thr Val Ser Lys Val Thr			
	380	385			390
Val Gln Ala Val	Thr Cys Glu Thr Thr	Val Glu Gln Leu Cys Pro			
	395	400			405
Phe His Lys Pro	Ala Ser His Cys Pro	Arg Val Tyr Cys Pro Arg			
	410	415			420
Asn Cys Met Gln	Ala Asn Pro His Tyr	Ala Arg Val Ile Gly Thr			
	425	430			435
Arg Val Tyr Ser	Asp Leu Ser Ser Ile	Cys Arg Ala Ala Val His			
	440	445			450
Ala Gly Val Val	Arg Asn His Gly Gly	Tyr Val Asp Val Met Pro			
	455	460			465

Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile
470 475 480

Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg
485 490 495

Val Phe Ala Val Val
500

<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365

ccaagagtat actgtcctcg 20

<210> 366

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 366

agcacagatt ttctctacag ccccc 25

<210> 367

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 367

aaccactcca gcatgtactg ctgc 24

<210> 368

<211> 50

<212> DNA

<213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe
 <400> 368
 ccattcagggt gttctgcccc tgtatgtaca cattatacac aggtcgtgtg 50
 <210> 369
 <211> 1685
 <212> DNA
 <213> Homo sapiens
 <400> 369
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 agagaaaagcc gagcagagct ggggtggcgtc tccgggccgc cgctccgacg 150
 ggccagcgcc ctccccatgt ccttgcctcc acgcgcgcc cctccggtca 200
 gcatgaggct cctggcggcc gcgctgctcc tgctgctgct ggcgctgtac 250
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 cgaggtcagg agcactgcct gcaccccaag ctgcagagca ccaagcgctt 450
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 aaaaaaaaaa aaagcctttc tttctcacag gcataagaca caaattatat 650
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<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

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Leu	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Ala	
				20				25					30	
Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys
				35				40						45
Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr
				50				55						60
Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val
				65				70						75
Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln
				80				85						90
Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys
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Arg	Arg	Val	Tyr	Glu	Glu									
				110										

<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

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<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373

ctccggtcag catgaggctc ctggcggccg ctgctcctgc tgctg 45

<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

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gcagcaaaaag gcaactatgg gtccttgat cagattcaag cactgcggtg 750
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atgctcagcg ccgtgggtcat gacctactgg acgaacttcg ccaaaactgg 1650
tgatccaaat caaccagttc ctcaggatac caagttcatt cacacaaaac 1700
ccaaccgctt tgaagaagtg gcctgggtcca agtataatcc caaagaccag 1750
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aacgaaagtg gctttctggt tggaactcgt tcctcatttg cacaacttga 1850
acgagatatt ccagtatgtt tcaacaacca caaaggttcc tccaccagac 1900
atgacatcat ttccctatgg caccggcgca tctcccgcca agatatggcc 1950
aaccacaaa cgccagcaa tcaactcctgc caacaatccc aaactactta 2000
aggaccctca caaacagggg cctgaggaca caactgtcct cattgaaacc 2050
aaacgagatt attccaccga attaagtgtc accattgccg tcggggcgctc 2100

				50					55					60
Ser	Pro	Pro	Thr	Gly 65	Glu	Arg	Arg	Phe	Gln 70	Pro	Pro	Glu	Pro	Pro 75
Ser	Ser	Trp	Thr	Gly 80	Ile	Arg	Asn	Thr	Thr 85	Gln	Phe	Ala	Ala	Val 90
Cys	Pro	Gln	His	Leu 95	Asp	Glu	Arg	Ser	Leu 100	Leu	His	Asp	Met	Leu 105
Pro	Ile	Trp	Phe	Thr 110	Ala	Asn	Leu	Asp	Thr 115	Leu	Met	Thr	Tyr	Val 120
Gln	Asp	Gln	Asn	Glu 125	Asp	Cys	Leu	Tyr	Leu 130	Asn	Ile	Tyr	Val	Pro 135
Thr	Glu	Asp	Gly	Ala 140	Asn	Thr	Lys	Lys	Asn 145	Ala	Asp	Asp	Ile	Thr 150
Ser	Asn	Asp	Arg	Gly 155	Glu	Asp	Glu	Asp	Ile 160	His	Asp	Gln	Asn	Ser 165
Lys	Lys	Pro	Val	Met 170	Val	Tyr	Ile	His	Gly 175	Gly	Ser	Tyr	Met	Glu 180
Gly	Thr	Gly	Asn	Met 185	Ile	Asp	Gly	Ser	Ile 190	Leu	Ala	Ser	Tyr	Gly 195
Asn	Val	Ile	Val	Ile 200	Thr	Ile	Asn	Tyr	Arg 205	Leu	Gly	Ile	Leu	Gly 210
Phe	Leu	Ser	Thr	Gly 215	Asp	Gln	Ala	Ala	Lys 220	Gly	Asn	Tyr	Gly	Leu 225
Leu	Asp	Gln	Ile	Gln 230	Ala	Leu	Arg	Trp	Ile 235	Glu	Glu	Asn	Val	Gly 240
Ala	Phe	Gly	Gly	Asp 245	Pro	Lys	Arg	Val	Thr 250	Ile	Phe	Gly	Ser	Gly 255
Ala	Gly	Ala	Ser	Cys 260	Val	Ser	Leu	Leu	Thr 265	Leu	Ser	His	Tyr	Ser 270
Glu	Gly	Leu	Phe	Gln 275	Lys	Ala	Ile	Ile	Gln 280	Ser	Gly	Thr	Ala	Leu 285
Ser	Ser	Trp	Ala	Val 290	Asn	Tyr	Gln	Pro	Ala 295	Lys	Tyr	Thr	Arg	Ile 300
Leu	Ala	Asp	Lys	Val 305	Gly	Cys	Asn	Met	Leu 310	Asp	Thr	Thr	Asp	Met 315
Val	Glu	Cys	Leu	Arg 320	Asn	Lys	Asn	Tyr	Lys 325	Glu	Leu	Ile	Gln	Gln 330
Thr	Ile	Thr	Pro	Ala 335	Thr	Tyr	His	Ile	Ala 340	Phe	Gly	Pro	Val	Ile 345

Asp Gly Asp Val	Ile Pro Asp Asp Pro	Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu	Asn Tyr Asp Ile Met	Leu Gly Val Asn Gln Gly	365	370	375
Glu Gly Leu Lys	Phe Val Asp Gly Ile	Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn	Asp Phe Asp Phe Ser	Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly	Tyr Pro Glu Gly Lys	Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met	Tyr Thr Asp Trp Ala	Asp Lys Glu Asn Pro Glu	425	430	435
Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn			

635	640	645
Asn Pro Lys His Ser Lys Asp Pro His	Lys Thr Gly Pro Glu Asp	
650	655	660
Thr Thr Val Leu Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu Leu	
665	670	675
Ser Val Thr Ile Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn Ile	
680	685	690
Leu Ala Phe Ala Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg His	
695	700	705
Glu Thr His Arg Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn Asp	
710	715	720
Ile Ala His Ile Gln Asn Glu Glu Ile	Met Ser Leu Gln Met Lys	
725	730	735
Gln Leu Glu His Asp His Glu Cys Glu	Ser Leu Gln Ala His Asp	
740	745	750
Thr Leu Arg Leu Thr Cys Pro Pro Asp	Tyr Thr Leu Thr Leu Arg	
755	760	765
Arg Ser Pro Asp Asp Ile Pro Leu Met	Thr Pro Asn Thr Ile Thr	
770	775	780
Met Ile Pro Asn Thr Leu Thr Gly Met	Gln Pro Leu His Thr Phe	
785	790	795
Asn Thr Phe Ser Gly Gly Gln Asn Ser	Thr Asn Leu Pro His Gly	
800	805	810
His Ser Thr Thr Arg Val		
815		

<210> 376
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 376
 ggcaagctac ggaaacgtca tcgtg 25

<210> 377
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccgggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

gggaaagatg gcggcgactc tgggaccct tgggtcgtgg cagcagtggc 50

ggcgatgttt gtcggtcgg gatgggtcca ggatgttact cttcttctt 100

ttgttgggt ctgggcagg gccacagcaa gtcggggcgg gtcaaacgtt 150

cgagtacttg aaacgggagc actcgctgtc gaagccctac cagggtgttg 200

gcacaggcag ttctcactg tggaatctga tgggcaatgc catggtgatg 250

accagttata tccgccttac ccagatatg caaagtaaac aggtgcctt 300

gtggaaccgg gtgccatgtt tctgagaga ctgggagttg caggtgcact 350

tcaaaatcca tggacaagga aagaagaatc tgcattggga tggcttggca 400

atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaaacat 450

ggacaaatth gtggggctgg gagtatttgt agacacctac ccaatgagg 500

agaagcagca agagcgggta ttcccctaca tctcagccat ggtgaacaac 550

ggctccctca gctatgatca tgagcgggat gggcggccta cagagctggg 600

aggctgcaca gccattgtcc gcaatcttca ttacgacacc ttcttgggtga 650

ttcgctacgt caagaggcat ttgacgataa tgatggatat tgatggcaag 700

catgagtggg gggactgcat tgaagtgcc ggagtccgcc tgccccgcgg 750

ctactacttc ggcacctcct ccatcactgg ggatctctca gataatcatg 800

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gaggaaaagc tccatcgaga tgtgttcttg ccctcagtgg acaatatgaa 900

gctgcctgag atgacagctc cactgccgcc cctgagtggc ctggccctct 950

tcctcatcgt ctttttctcc ctggtgtttt ctgtatttgc catagtcatt 1000

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 ctgagccctc ctgctgccac cacttttgtg actgtcacc c atgaggtatg 1100
 gaaggagcag gcactggcct gagcatgcag cctggagagt gttcttgtct 1150
 ctagcagctg gttggggact atattctgtc actggagttt tgaatgcagg 1200
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 aagccacca cccagggca atgctgctgt gatgtgcctt tccctgcagt 1300
 ccttccatgt gggagcagag gtgtgaagag aatttacgtg gttgtgatgc 1350
 caaaatcaca gaacagaatt tcatagccca ggctgccgtg ttgtttgact 1400
 cagaaggccc ttctacttca gttttgaatc caciaagaat taaaaactgg 1450
 taacaccaca ggctttctga ccatccattc gttgggtttt gcatttgacc 1500
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 caaaagcaac atttgtcatg tggctgacc atgtggagat gtttctggac 1950
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 ccactttgag tgctgaaagt gtaaggaagc tttcttctta caccttgggc 2050
 ttggatattg ccagagaag aaatttggct ttttttttct taatggacaa 2100
 gagacagtgt ctgtttctcat gttccaagtc tgagagcaac agaccctcat 2150
 catctgtgcc tggaagagtt cactgtcatt gagcagcaca gcctgagtgc 2200
 tggcctctgt caacccttat tccactgcct tatttgacaa ggggttacat 2250
 gctgtcacc ttactgccct gggattaaat cagttacagg ccagagtctc 2300
 cttggagggc ctggaactct gagtctctct atgaacctct gtagcctaaa 2350
 tgaaattctt aaaatcaccg atggaaccaa aaaaaaaaaa aaaaagggcg 2400
 gccgcgactc tagagtcgac ctgcagtagg gataacagg taataagctt 2450

ggccgccatg g 2461

<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

Met	Ala	Ala	Thr	Leu	Gly	Pro	Leu	Gly	Ser	Trp	Gln	Gln	Trp	Arg	
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Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu	
				20					25					30	
Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly	
				35					40					45	
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro	
				50					55					60	
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met	
				65					70					75	
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp	
				80					85					90	
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe	
				95					100					105	
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln	
				110					115					120	
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr	
				125					130					135	
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys	
				140					145					150	
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu	
				155					160					165	
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn	
				170					175					180	
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr	
				185					190					195	
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp	
				200					205					210	
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met	
				215					220					225	
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val	
				230					235					240	
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser	
				245					250					255	

Ile Thr Gly Asp	Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys	
260	265	270
Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu		
275	280	285
His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro		
290	295	300
Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe		
305	310	315
Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val		
320	325	330
Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys		
335	340	345
Arg Phe Tyr		

<210> 381
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 381
 ccttgggtcg tggcagcagt gg 22

<210> 382
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 382
 cactctocag gctgcatgct cagg 24

<210> 383
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 383
 gtcaaacggtt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384
 <211> 3150
 <212> DNA
 <213> Homo sapiens

<400> 384

ccgagccggg cgcgccagcga cggagctggg gccggcctgg gaccatgggc 50
 gtgagtgcaa tctacggatc agtctctgat ggtgggtcgt taacctcagt 100
 ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150
 tggggctctgg ctccagaattc ctgcagctgg tgaaaatctg ttttctagaa 200
 gaggtttaat taatgcctgc agtctgacat gttcccgatt tgaggtgaaa 250
 ccatgaagag aaaatagaat acttaataat gcttttccgc aaccgcttct 300
 tgctgctgct ggccctggct gcgctgctgg cctttgtgag cctcagcctg 350
 cagttcttcc acctgatccc ggtgtcgact cctaagaatg gaatgagtag 400
 caagagtoga aagagaatca tgcccgaccc tgtgacggag ccccctgtga 450
 cagaccccggt ttatgaagct cttttgtact gcaacatccc cagtgtggcc 500
 gagcgccagca tggaagggtca tgccccgcat cattttaagc tggctctcagt 550
 gcatgtgttc attogccacg gagacaggta cccactgtat gtcattccca 600
 aaacaaagcg accagaaatt gactgcactc tgggtggctaa caggaaaccg 650
 tatcacccaa aactggaagc tttcattagt cacatgtcaa aaggatccgg 700
 agcctctttc gaaagcccct tgaactcctt gcctctttac ccaaaccacc 750
 cattgtgtga gatgggagag ctccacacaga caggagtgtg gcagcatttg 800
 cagaacggtc agctgctgag ggatatctat ctaaagaaac acaaactcct 850
 gcccaatgat tgggtctgcag accagctcta tttagagacc actgggaaaa 900
 gccggaccct acaaagtggg ctggccttgc tttatggctt tctcccagat 950
 tttgactgga agaagattta tttcaggcac cagccaagtg cgctgttctg 1000
 ctctggaagc tgctattgcc cggtaagaaa ccagtatctg gaaaaggagc 1050
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 tacggggaga tggccaagat cgtggatgtc cccaccaagc agcttagagc 1150
 tgccaacccc atagactcca tgctctgcc aattctgccac aatgtcagct 1200
 ttccctgtac cagaaatggc tgtgttgaca tggagcactt caaggtaatt 1250
 aagaccatc agatcgagga tgaaagggaa agacgggaga agaaattgta 1300
 cttcgggtat tctctcctgg gtgcccaccc catcctgaac caaaccatcg 1350
 gccggatgca gcgtgccacc gagggcagga aagaagagct ctttgccctc 1400
 tactctgctc atgatgtcac tctgtcacca gttctcagtg ccttgggcct 1450

ttcagaagcc aggttcccaa ggtttgcagc caggttgatc tttgagcttt 1500
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 taagggtaga agattattgc tttttaaagg ctaaattattg tttgtgggaa 1850
 ccacagatgg ttgggggtga acagtaagca cattgctgca atgtggtacg 1900
 tgaattgctt ggtacaaaat ggccagttca cagaggaata gaaggtactt 1950
 tatcatagcc agacttcgct tagaatgcca gaataatata gttcaagacc 2000
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 tgtgatggaa ccagcacacc tcaacccaaa tttttttaat cttagacatt 2100
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 ctgggttccc aggccagaca aaacagatgg tgaccagact tggcccctgg 2350
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attgattttt aaatgcgttt ttggaagaac ttgctatta ggtagtttac 2950
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 tgatttctga actaatgggtg ctaattcaga gaaatggaaa gtgaaagtga 3050
 gattctctgt tgtcatcggc attccaactt tttctctttg tttttgtcca 3100
 gtgttgcatt tgaatatgtc tgtttctata aataaatttt ttaagaataa 3150

<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

Met	Leu	Phe	Arg	Asn	Arg	Phe	Leu	Leu	Leu	Leu	Ala	Leu	Ala	Ala	1	5	10	15
Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile	20	25	30	
Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys	35	40	45	
Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro	50	55	60	
Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu	65	70	75	
Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser	80	85	90	
Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val	95	100	105	
Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala	110	115	120	
Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His	125	130	135	
Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser	140	145	150	
Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu	155	160	165	
Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu	170	175	180	
Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp	185	190	195	
Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr	200	205	210	

<220>
<223> Synthetic oligonucleotide probe

<400> 386
ccaagcagct tagagctcca gacc 24

<210> 387
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 387
ttccctatgc tctgtattgg catgg 25

<210> 388
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 388
gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389
<211> 3313
<212> DNA
<213> Homo sapiens

<400> 389
aaaaaagctc actaaagttt ctattagagc gaatacggta gatttccatc 50
cccttttgaa gaacagtact gtggagctat ttaagagata aaaacgaaat 100
atcctttctg ggagttcaag attgtgcagt aattggttag gactctgagc 150
gocgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200
cacgcgcctg aagcacaaag cagatagcta ggaatgaacc atccctggga 250
gtatgtggaa acaacggagg agctctgact tcccaactgt cccattctat 300
gggcgaagga actgctcctg acttcagtgg ttaagggcag aattgaaaat 350
aattctggag gaagataaga atgattcctg cgcgactgca ccgggactac 400
aaagggcttg tcctgctggg aatcctcctg gggactctgt gggagaccgg 450
atgcacccag atacgtatt cagttccgga agagctggag aaaggctcta 500
gggtgggcga catctccagg gacctggggc tggagccccg ggagctcgcg 550
gagcgcggag tccgcatcat cccagaggt aggacgcagc ttttcgccct 600

Met	Ile	Pro	Ala	Arg	Leu	His	Arg	Asp	Tyr	Lys	Gly	Leu	Val	Leu			
1				5					10					15			
Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln			
				20					25					30			
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val			
				35					40					45			
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala			
				50					55					60			
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe			
				65					70					75			
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile			
				80					85					90			
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn			
				95					100					105			
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu			
				110					115					120			
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu			
				125					130					135			
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met			
				140					145					150			
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn			
				155					160					165			
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu			
				170					175					180			
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val			
				185					190					195			
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu			
				200					205					210			
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr			
				215					220					225			
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro			
				230					235					240			
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu			
				245					250					255			
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp			
				260					265					270			
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp			
				275					280					285			
Asp	Lys	Ala	Ala	Gln	Val	Phe	Lys	Leu	Asp	Cys	Asn	Ser	Gly	Thr			

				290					295					300
Ile	Ser	Thr	Ile	Gly 305	Glu	Leu	Asp	His	Glu 310	Glu	Ser	Gly	Phe	Tyr 315
Gln	Met	Glu	Val	Gln 320	Ala	Met	Asp	Asn	Ala 325	Gly	Tyr	Ser	Ala	Arg 330
Ala	Lys	Val	Leu	Ile 335	Thr	Val	Leu	Asp	Val 340	Asn	Asp	Asn	Ala	Pro 345
Glu	Val	Val	Leu	Thr 350	Ser	Leu	Ala	Ser	Ser 355	Val	Pro	Glu	Asn	Ser 360
Pro	Arg	Gly	Thr	Leu 365	Ile	Ala	Leu	Leu	Asn 370	Val	Asn	Asp	Gln	Asp 375
Ser	Glu	Glu	Asn	Gly 380	Gln	Val	Ile	Cys	Phe 385	Ile	Gln	Gly	Asn	Leu 390
Pro	Phe	Lys	Leu	Glu 395	Lys	Ser	Tyr	Gly	Asn 400	Tyr	Tyr	Ser	Leu	Val 405
Thr	Asp	Ile	Val	Leu 410	Asp	Arg	Glu	Gln	Val 415	Pro	Ser	Tyr	Asn	Ile 420
Thr	Val	Thr	Ala	Thr 425	Asp	Arg	Gly	Thr	Pro 430	Pro	Leu	Ser	Thr	Glu 435
Thr	His	Ile	Ser	Leu 440	Asn	Val	Ala	Asp	Thr 445	Asn	Asp	Asn	Pro	Pro 450
Val	Phe	Pro	Gln	Ala 455	Ser	Tyr	Ser	Ala	Tyr 460	Ile	Pro	Glu	Asn	Asn 465
Pro	Arg	Gly	Val	Ser 470	Leu	Val	Ser	Val	Thr 475	Ala	His	Asp	Pro	Asp 480
Cys	Glu	Glu	Asn	Ala 485	Gln	Ile	Thr	Tyr	Ser 490	Leu	Ala	Glu	Asn	Thr 495
Ile	Gln	Gly	Ala	Ser 500	Leu	Ser	Ser	Tyr	Val 505	Ser	Ile	Asn	Ser	Asp 510
Thr	Gly	Val	Leu	Tyr 515	Ala	Leu	Ser	Ser	Phe 520	Asp	Tyr	Glu	Gln	Phe 525
Arg	Asp	Leu	Gln	Val 530	Lys	Val	Met	Ala	Arg 535	Asp	Asn	Gly	His	Pro 540
Pro	Leu	Ser	Ser	Asn 545	Val	Ser	Leu	Ser	Leu 550	Phe	Val	Leu	Asp	Gln 555
Asn	Asp	Asn	Ala	Pro 560	Glu	Ile	Leu	Tyr	Pro 565	Ala	Leu	Pro	Thr	Asp 570
Gly	Ser	Thr	Gly	Val 575	Glu	Leu	Ala	Pro	Arg 580	Ser	Ala	Glu	Pro	Gly 585

Tyr	Leu	Val	Thr	Lys	Val	Val	Ala	Val	Asp	Arg	Asp	Ser	Gly	Gln	
				590					595					600	
Asn	Ala	Trp	Leu	Ser	Tyr	Arg	Leu	Leu	Lys	Ala	Ser	Glu	Pro	Gly	
				605					610					615	
Leu	Phe	Ser	Val	Gly	Leu	His	Thr	Gly	Glu	Val	Arg	Thr	Ala	Arg	
				620					625					630	
Ala	Leu	Leu	Asp	Arg	Asp	Ala	Leu	Lys	Gln	Ser	Leu	Val	Val	Ala	
				635					640					645	
Val	Gln	Asp	His	Gly	Gln	Pro	Pro	Leu	Ser	Ala	Thr	Val	Thr	Leu	
				650					655					660	
Thr	Val	Ala	Val	Ala	Asp	Ser	Ile	Pro	Gln	Val	Leu	Ala	Asp	Leu	
				665					670					675	
Gly	Ser	Leu	Glu	Ser	Pro	Ala	Asn	Ser	Glu	Thr	Ser	Asp	Leu	Thr	
				680					685					690	
Leu	Tyr	Leu	Val	Val	Ala	Val	Ala	Ala	Val	Ser	Cys	Val	Phe	Leu	
				695					700					705	
Ala	Phe	Val	Ile	Leu	Leu	Leu	Ala	Leu	Arg	Leu	Arg	Arg	Trp	His	
				710					715					720	
Lys	Ser	Arg	Leu	Leu	Gln	Ala	Ser	Gly	Gly	Gly	Leu	Thr	Gly	Ala	
				725					730					735	
Pro	Ala	Ser	His	Phe	Val	Gly	Val	Asp	Gly	Val	Gln	Ala	Phe	Leu	
				740					745					750	
Gln	Thr	Tyr	Ser	His	Glu	Val	Ser	Leu	Thr	Thr	Asp	Ser	Arg	Lys	
				755					760					765	
Ser	His	Leu	Ile	Phe	Pro	Gln	Pro	Asn	Tyr	Ala	Asp	Met	Leu	Val	
				770					775					780	
Ser	Gln	Glu	Ser	Phe	Glu	Lys	Ser	Glu	Pro	Leu	Leu	Leu	Ser	Gly	
				785					790					795	
Asp	Ser	Val	Phe	Ser	Lys	Asp	Ser	His	Gly	Leu	Ile	Glu	Val	Ser	
				800					805					810	
Leu	Tyr	Gln	Ile	Phe	Phe	Leu	Phe	Phe	Phe	Asn	Cys	Ser	Val	Ser	
				815					820					825	
Gln	Ala	Gly	Val	Gln	Arg	Tyr	Asp	His	Ser	Ser	Leu	Arg	Pro	Gln	
				830					835					840	
Thr	Pro	Arg	Leu	Lys	Gln	Leu	Ser	His	Leu	Cys	Leu	Arg	Cys	Asn	
				845					850					855	
Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr	
				860					865					870	
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu	

	875		880		885
Ser Cys Thr Asp	Gly Ser Leu Thr Pro	Val Ile Pro Val Leu Trp			
	890	895	900		
Glu Ala Glu Ala	Gly Gly Ser Pro Glu	Val Gly Ser Leu Arg Pro			
	905	910	915		

Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcgggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

cccagttaaa aggctccaga atcgtgtacc aggagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150

ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200

gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250
 aggaggacaa ggtgctgggg ggtcatgagt gccaacccca ttcgcagcct 300
 tggcaggcgg ccttggtcca gggccagcaa ctactctgtg gcggtgtcct 350
 tgtaggtggc aactgggtcc ttacagctgc ccactgtaaa aaaccgaaat 400
 acacagtacg cctgggagac cacagcctac agaataaaga tggcccagag 450
 caagaaatac ctgtggttca gtccatccca caccctgtct acaacagcag 500
 cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgctgtacc 550
 aggcattcct ggggtccaaa gtgaagccca tcagcctggc agatcattgc 600
 acccagcctg gccagaagtg caccgtctca ggctggggca ctgtcaccag 650
 tccccgagag aattttcctg acactctcaa ctgtgcagaa gtaaaaatct 700
 ttccccagaa gaagtgtgag gatgcttacc cggggcagat cacagatggc 750
 atggtctgtg caggcagcag caaaggggct gacacgtgcc agggcgattc 800
 tggaggcccc ctggtgtgtg atggtgcact ccagggcata acatcctggg 850
 gctcagaccc ctgtgggagg tccgacaaac ctggcgtcta taccaacata 900
 tgccgctacc tggactggat caagaagata ataggcagca agggctgatt 950
 ctaggataag cactagatct cccttaataa actcacaact ctctgggttc 999

<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
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Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30
Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60
Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75
Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn
			80						85					90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro
			95						100					105

His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp
				110					115					120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys
				125					130					135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln
				140					145					150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu
				155					160					165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro
				170					175					180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly
				185					190					195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly
				200					205					210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile
				215					220					225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly
				230					235					240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile
				245					250					255
Ile	Gly	Ser	Lys	Gly										
				260										

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gccc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

ggcgccggtg caccgggagg gctgagcgcc tcctgcggcc cggcctgcgc 50

gccccggccc gccgcgccgc ccacgcccc accccggccc gcgcccccta 100

gccccgccc gggcccgccg ccgcgccgc gccaggtga gcgtccgcc 150

cgccgcgagg ccccgcccc gcccgcccc gcccgcccc ggccggcggg 200

ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250

tcctcctccc ggccggccgc gctgcgagcg ccccgccagt ccgcgccgc 300

gccgccctcg cctgtgcgc cctgcgcgc ctgcgcaccc gcggcccgag 350

cccagccaga gccgggagg ggcgagcgcg ccgagcctcg tcccgcgcc 400

gggcccgggc cgggcccgtg cggcgccgc tggatgcgga cccggccgcg 450

gggagacggg cggccgcccc gaaacgactt tcagtccccg acgcgccccg 500

cccaaccct acgatgaaga gggcgccgc tggaggaggc cggctgctgg 550

catgggtgct gtggctgcag gcctggcagg tggcagcccc atgccagggt 600

gcctgcgtat gctacaatga gcccaagggt acgacaagct gccccagca 650

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tcctgcacgg caaccgcac tcgcatgtgc cagctgccag cttccgtgcc 750

tgccgcaacc tcaccatcct gtggctgcac tcgaatgtgc tggcccgaat 800

tgatgcggct gccttactg gcctggccct cctggagcag ctggacctca 850

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ctcacacacc tcttctgca cggcaaccgc atctccagcg tgcccagcg 1100

cgccttccgt gggctgcaca gcctcgaccg tctcctactg caccagaacc 1150
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 acactctatc tgtttgccaa caatctatca gcgctgcca ctgaggccct 1250
 ggccccctg cgtgccctgc agtacctgag gctcaacgac aaccctggg 1300
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 ggctcctcct ccgaggtgcc ctgcagcctc ccgcaacgcc tggctggccg 1400
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 ctggggcttc ccaagtgtg ccagccagat gccgctgaca aggcctcagt 1550
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 aatgactcac cttttgggac tctgcctggc tctgctgagc ccccgctcac 1700
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 ctgcgccgag gccaggtgt tcaogcaaga accgcacccg cagccactgc 1800
 cgtctgggcc aggcaggcag cgggggtggc gggactggtg actcagaagg 1850
 ctcaggtgcc ctaccagacc tcacctgcag cctcaccccc ctgggcctgg 1900
 cgctggtgct gtggacagtg cttgggccct gctgaccccc agcggacaca 1950
 agagcgtgct cagcagccag gtgtgtgtac atacggggtc tctctccacg 2000
 ccgccaagcc agccgggcgg ccgaccctg gggcaggcca ggccaggtcc 2050
 tccctgatgg acgcctgccg ccgcccaccc ccatctccac cccatcatgt 2100
 ttacaggggt cggcggcagc gtttgttcca gaacgccgcc tcccaccag 2150
 atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200
 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

Met	Lys	Arg	Ala	Ser	Ala	Gly	Gly	Ser	Arg	Leu	Leu	Ala	Trp	Val
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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala
			20						25					30

Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	35	40	45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	50	55	60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	65	70	75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	80	85	90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	95	100	105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	110	115	120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	125	130	135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	140	145	150
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	155	160	165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	170	175	180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	185	190	195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	200	205	210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	215	220	225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	230	235	240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	245	250	255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	260	265	270
Leu	Trp	Ala	Trp	Leu	Gln	Lys	Phe	Arg	Gly	Ser	Ser	Ser	Glu	Val	275	280	285
Pro	Cys	Ser	Leu	Pro	Gln	Arg	Leu	Ala	Gly	Arg	Asp	Leu	Lys	Arg	290	295	300
Leu	Ala	Ala	Asn	Asp	Leu	Gln	Gly	Cys	Ala	Val	Ala	Thr	Gly	Pro	305	310	315
Tyr	His	Pro	Ile	Trp	Thr	Gly	Arg	Ala	Thr	Asp	Glu	Glu	Pro	Leu			

05976104-10501

	320		325		330
Gly Leu Pro Lys	Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala	Ser		
	335		340		345
Val Leu Glu Pro	Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu	Lys		
	350		355		360
Gly Arg Val Pro	Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser	Gly		
	365		370		375
Pro Arg His Ile	Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly	Ser		
	380		385		390
Ala Glu Pro Pro	Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu	Pro		
	395		400		405
Pro Gly Phe Pro	Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys	Ser		
	410		415		420
Arg Lys Asn Arg	Thr Arg Ser His Cys	Arg Leu Gly Gln Ala	Gly		
	425		430		435
Ser Gly Gly Gly	Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala	Leu		
	440		445		450
Pro Ser Leu Thr	Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu	Val		
	455		460		465
Leu Trp Thr Val	Leu Gly Pro Cys				
	470				

<210> 401
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 401
 tggctgccct gcagtacctc tacc 24

<210> 402
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 402
 ccctgcaggt cattggcagc tagg 24

<210> 403
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 403
aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404
<211> 2738
<212> DNA
<213> Homo sapiens

<400> 404
ggaagtccac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50
ggagaggact actcactggc atatttctga ggtatctgta gaataaccac 100
agcctcagat actggggact ttacagtccc acagaaccgt cctcccagga 150
agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgaga 200
caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250
cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300
cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350
tccaggcggg gggttagggt tgtttccaga gggaacaaac tacatttgca 400
gctcaatcag gagaccgagg atttgttgct aaatgagaaa ttggaccgtg 450
aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500
ctagagagtc ccttcgagtt ttttcaagct gagctgcaag taatagacat 550
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Asp	Thr	Gly	Val	Asn 275	Gly	Glu	Ile	Ser	Tyr 280	Ser	Leu	Phe	Gln	Ala 285
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Lys	Cys	Thr	Val	Leu 335	Ile	Gln	Val	Ile	Asp 340	Val	Asn	Asp	His	Ala 345
Pro	Glu	Val	Thr	Met 350	Ser	Ala	Phe	Thr	Ser 355	Pro	Ile	Pro	Glu	Asn 360
Ala	Pro	Glu	Thr	Val 365	Val	Ala	Leu	Phe	Ser 370	Val	Ser	Asp	Leu	Asp 375
Ser	Gly	Glu	Asn	Gly 380	Lys	Ile	Ser	Cys	Ser 385	Ile	Gln	Glu	Asp	Leu 390
Pro	Phe	Leu	Leu	Lys 395	Ser	Ala	Glu	Asn	Phe 400	Tyr	Thr	Leu	Leu	Thr 405
Glu	Arg	Pro	Leu	Asp 410	Arg	Glu	Ser	Arg	Ala 415	Glu	Tyr	Asn	Ile	Thr 420
Ile	Thr	Val	Thr	Asp 425	Leu	Gly	Thr	Pro	Met 430	Leu	Ile	Thr	Gln	Leu 435
Asn	Met	Thr	Val	Leu 440	Ile	Ala	Asp	Val	Asn 445	Asp	Asn	Ala	Pro	Ala 450
Phe	Thr	Gln	Thr	Ser 455	Tyr	Thr	Leu	Phe	Val 460	Arg	Glu	Asn	Asn	Ser 465
Pro	Ala	Leu	His	Ile 470	Arg	Ser	Val	Ser	Ala 475	Thr	Asp	Arg	Asp	Ser 480
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Gly	His	Leu	Phe	Ala 515	Leu	Arg	Ser	Leu	Asp 520	Tyr	Glu	Ala	Leu	Gln 525

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Pro	Cys	Thr	Glu	Leu	Val	Pro	Arg	Ala	Ala	Glu	Pro	Gly	Tyr	Leu	
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Val	Thr	Lys	Val	Val	Ala	Val	Asp	Gly	Asp	Ser	Gly	Gln	Asn	Ala	
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Trp	Leu	Ser	Tyr	Gln	Leu	Leu	Lys	Ala	Thr	Glu	Leu	Gly	Leu	Phe	
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Ser	Glu	Arg	Asp	Ala	Ala	Lys	His	Arg	Leu	Val	Val	Leu	Val	Lys	
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Val	Val	Ala	Leu	Ala	Ser	Val	Ser	Ser	Leu	Phe	Leu	Phe	Ser	Val	
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Leu	Leu	Phe	Val	Ala	Val	Arg	Leu	Cys	Arg	Arg	Ser	Arg	Ala	Ala	
				710					715					720	
Ser	Val	Gly	Arg	Cys	Leu	Val	Pro	Glu	Gly	Pro	Leu	Pro	Gly	His	
				725					730					735	
Leu	Val	Asp	Met	Ser	Gly	Thr	Arg	Thr	Leu	Ser	Gln	Ser	Tyr	Gln	
				740					745					750	
Tyr	Glu	Val	Cys	Leu	Ala	Gly	Gly	Ser	Gly	Thr	Asn	Glu	Phe	Lys	
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Phe	Leu	Lys	Pro	Ile	Ile	Pro	Asn	Phe	Pro	Pro	Gln	Cys	Pro	Gly	
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Lys	Glu	Ile	Gln	Gly	Asn	Ser	Thr	Phe	Pro	Asn	Asn	Phe	Gly	Phe	
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<210> 406

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<220>
<223> Synthetic oligonucleotide probe

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<400> 407
agcgttgtca ttgacatcgg cg 22
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<210> 408
<211> 50
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic oligonucleotide probe

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<210> 409
<211> 1379
<212> DNA
<213> Homo sapiens
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  cggtcgacga  ccgccccgcg  tcatgcggct  cctcggctgg  tggcaagtat  150
  tgctgtgggt  gctgggactt  cccgtccgcg  gcgtggagggt  tgcagaggaa  200
  agtggtcgct  tatggtcaga  ggagcagcct  gtcaccctc  tccaggtggg  250
  ggctgtgtac  ctgggtgagg  aggagctcct  gcatgaccgc  atgggccagg  300
  acagggcagc  agaagaggcc  aatgcggtgc  tggggctgga  caccaaggcc  350
  gatcacatgg  tgatgctgtc  tgtgattcct  ggggaagctg  aggacaaagt  400
  gagttcagag  cctagcggcg  tcacctgtgg  tgctggagga  gcggaggact  450
  caagggtgcaa  cgtccgagag  agccttttct  ctctggatgg  cgctggagca  500
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<210> 410
 <211> 360
 <212> PRT
 <213> Homo sapiens

<400> 410
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 35 40 45
 Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly
 50 55 60
 Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala
 65 70 75
 Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His

	80		85		90
Met Val Met Leu Ser Val Ile Pro Gly	95	Glu Ala Glu Asp Lys Val	100		105
Ser Ser Glu Pro Ser Gly Val Thr Cys	110	Gly Ala Gly Gly Ala Glu	115		120
Asp Ser Arg Cys Asn Val Arg Glu Ser	125	Leu Phe Ser Leu Asp Gly	130		135
Ala Gly Ala His Phe Pro Asp Arg Glu	140	Glu Glu Tyr Tyr Thr Glu	145		150
Pro Glu Val Ala Glu Ser Asp Ala Ala	155	Pro Thr Glu Asp Ser Asn	160		165
Asn Thr Glu Ser Leu Lys Ser Pro Lys	170	Val Asn Cys Glu Glu Arg	175		180
Asn Ile Thr Gly Leu Glu Asn Phe Thr	185	Leu Lys Ile Leu Asn Met	190		195
Ser Gln Asp Leu Met Asp Phe Leu Asn	200	Pro Asn Gly Ser Asp Cys	205		210
Thr Leu Val Leu Phe Tyr Thr Pro Trp	215	Cys Arg Phe Ser Ala Ser	220		225
Leu Ala Pro His Phe Asn Ser Leu Pro	230	Arg Ala Phe Pro Ala Leu	235		240
His Phe Leu Ala Leu Asp Ala Ser Gln	245	His Ser Ser Leu Ser Thr	250		255
Arg Phe Gly Thr Val Ala Val Pro Asn	260	Ile Leu Leu Phe Gln Gly	265		270
Ala Lys Pro Met Ala Arg Phe Asn His	275	Thr Asp Arg Thr Leu Glu	280		285
Thr Leu Lys Ile Phe Ile Phe Asn Gln	290	Thr Gly Ile Glu Ala Lys	295		300
Lys Asn Val Val Val Thr Gln Ala Asp	305	Gln Ile Gly Pro Leu Pro	310		315
Ser Thr Leu Ile Lys Ser Val Asp Trp	320	Leu Leu Val Phe Ser Leu	325		330
Phe Phe Leu Ile Ser Phe Ile Met Tyr	335	Ala Thr Ile Arg Thr Glu	340		345
Ser Ile Arg Trp Leu Ile Pro Gly Gln	350	Glu Gln Glu His Val Glu	355		360

<210> 411
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 411
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<210> 412
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 412
ccacatgttc ctgctcttgc cctgg 25

<210> 413
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 413
cggtagtgcac tgcactctag tctgtttta caccctgtgg tgccg 45

<210> 414
<211> 1196
<212> DNA
<213> Homo sapiens

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<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

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Pro	Asp	Phe	Ser	Tyr	Lys	Arg	Ser	Asn	Cys	Lys	Pro	Ile	Pro	Val
				35					40					45
Asn	Leu	Gln	Leu	Cys	His	Gly	Ile	Glu	Tyr	Gln	Asn	Met	Arg	Leu
				50					55					60
Pro	Asn	Leu	Leu	Gly	His	Glu	Thr	Met	Lys	Glu	Val	Leu	Glu	Gln
				65					70					75
Ala	Gly	Ala	Trp	Ile	Pro	Leu	Val	Met	Lys	Gln	Cys	His	Pro	Asp
				80					85					90
Thr	Lys	Lys	Phe	Leu	Cys	Ser	Leu	Phe	Ala	Pro	Val	Cys	Leu	Asp
				95					100					105
Asp	Leu	Asp	Glu	Thr	Ile	Gln	Pro	Cys	His	Ser	Leu	Cys	Val	Gln
				110					115					120
Val	Lys	Asp	Arg	Cys	Ala	Pro	Val	Met	Ser	Ala	Phe	Gly	Phe	Pro
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Trp	Pro	Asp	Met	Leu	Glu	Cys	Asp	Arg	Phe	Pro	Gln	Asp	Asn	Asp	
				140					145					150	
Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	Leu	Leu	Pro	Ala	Thr	
				155					160					165	
Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys	Asn	Lys	Asn	Asp	
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Asp	Asp	Asn	Asp	Ile	Met	Glu	Thr	Leu	Cys	Lys	Asn	Asp	Phe	Ala	
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Lys	Ile	Ile	Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	Asn	
				215					220					225	
Gly	Val	Ser	Glu	Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	
				230					235					240	
Asp	Ser	Leu	Gln	Cys	Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	
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Pro	Tyr	Leu	Val	Met	Gly	Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	
				260					265					270	
Thr	Ser	Val	Lys	Arg	Trp	Gln	Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	
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<210> 416

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 416

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<210> 417

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417

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<210> 418

<211> 47

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 418

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<210> 419

<211> 1830

<212> DNA

<213> Homo sapiens

<400> 419

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Gly Thr Gln Asn	Pro Phe Ala Phe Leu	Met Gly Gly Gln Ser	Leu		
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Cys Ala Leu Ala	Gln Ser Leu Val Ile	Phe Ser Pro Ala Lys	Leu		
	140	145		150	
Ala Ala Leu Trp	Phe Pro Glu His Gln	Arg Ala Thr Ala Asn	Met		
	155	160		165	
Leu Ala Thr Met	Ser Asn Pro Leu Gly	Val Leu Val Ala Asn	Val		
	170	175		180	
Leu Ser Pro Val	Leu Val Lys Lys Gly	Glu Asp Ile Pro Leu	Met		
	185	190		195	
Leu Gly Val Tyr	Thr Ile Pro Ala Gly	Val Val Cys Leu Leu	Ser		
	200	205		210	
Thr Ile Cys Leu	Trp Glu Ser Val Pro	Pro Thr Pro Pro Ser	Ala		
	215	220		225	
Gly Ala Ala Ser	Ser Thr Ser Glu Lys	Phe Leu Asp Gly Leu	Lys		
	230	235		240	
Leu Gln Leu Met	Trp Asn Lys Ala Tyr	Val Ile Leu Ala Val	Cys		
	245	250		255	
Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala Leu	Leu		
	260	265		270	
Glu Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe Ser	Gly		
	275	280		285	
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly Ala	Leu		
	290	295		300	
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr Glu	Ala		
	305	310		315	
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val Pro	Phe		
	320	325		330	
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu Ala	Ala		
	335	340		345	
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly Pro	Val		
	350	355		360	
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly Glu	Gly		
	365	370		375	
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu Gly	Ile		
	380	385		390	
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg Ser	Glu		
	395	400		405	

Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu Asp Trp
410 415 420

Thr Val Ser Leu Leu Leu Met Ala Gly Leu Cys Thr Phe Phe Ser
425 430 435

Cys Ile Leu Ala Val Phe Phe His Thr Pro Tyr Arg Arg Leu Gln
440 445 450

Ala Glu Ser Gly Glu Pro Pro Ser Thr Arg Asn Ala Val Gly Gly
455 460 465

Ala Asp Ser Gly Pro Gly Val Asp Arg Gly Gly Ala Gly Arg Ala
470 475 480

Gly Val Leu Gly Pro Ser Thr Ala Thr Pro Glu Cys Thr Ala Arg
485 490 495

Gly Ala Ser Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro
500 505 510

Ala Cys His Arg Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr
515 520 525

Asp Ala Pro Ser Arg Pro Gly Arg Leu Ala Gly Arg Val Gln Ala
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Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser
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Pro Trp Val Ile Thr
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<210> 421

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

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<210> 422

<211> 25

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<223> Synthetic oligonucleotide probe

<400> 422

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<210> 423

<211> 43

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 423

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<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

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 aaaaaaaaaa aaa 4313

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 <211> 1184
 <212> PRT
 <213> Homo sapiens

<400> 425
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 Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val
 35 40 45
 Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg
 50 55 60
 Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu
 65 70 75
 Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg
 80 85 90
 Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu
 95 100 105
 Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His
 110 115 120
 Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe
 125 130 135
 Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu
 140 145 150
 Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly
 155 160 165
 Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe
 170 175 180
 Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu
 185 190 195

	485		490		495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val	Ala His Leu Val	Ala Ile		
	500	505	510		
Asp Ser Asn Thr	Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn	Tyr		
	515	520	525		
Glu Glu Met Ala	Gly Phe Glu Phe Gln	Val Ile Ala Glu Asp	Ser		
	530	535	540		
Gly Gln Pro Met	Leu Ala Ser Ser Val	Ser Val Trp Val Ser	Leu		
	545	550	555		
Leu Asp Ala Asn	Asp Asn Ala Pro Glu	Val Val Gln Pro Val	Leu		
	560	565	570		
Ser Asp Gly Lys	Ala Ser Leu Ser Val	Leu Val Asn Ala Ser	Thr		
	575	580	585		
Gly His Leu Leu	Val Pro Ile Glu Thr	Pro Asn Gly Leu Gly	Pro		
	590	595	600		
Ala Gly Thr Asp	Thr Pro Pro Leu Ala	Thr His Ser Ser Arg	Pro		
	605	610	615		
Phe Leu Leu Thr	Thr Ile Val Ala Arg	Asp Ala Asp Ser Gly	Ala		
	620	625	630		
Asn Gly Glu Pro	Leu Tyr Ser Ile Arg	Asn Gly Asn Glu Ala	His		
	635	640	645		
Leu Phe Ile Leu	Asn Pro His Thr Gly	Gln Leu Phe Val Asn	Val		
	650	655	660		
Thr Asn Ala Ser	Ser Leu Ile Gly Ser	Glu Trp Glu Leu Glu	Ile		
	665	670	675		
Val Val Glu Asp	Gln Gly Ser Pro Pro	Leu Gln Thr Arg Ala	Leu		
	680	685	690		
Leu Arg Val Met	Phe Val Thr Ser Val	Asp His Leu Arg Asp	Ser		
	695	700	705		
Ala Arg Lys Pro	Gly Ala Leu Ser Met	Ser Met Leu Thr Val	Ile		
	710	715	720		
Cys Leu Ala Val	Leu Leu Gly Ile Phe	Gly Leu Ile Leu Ala	Leu		
	725	730	735		
Phe Met Ser Ile	Cys Arg Thr Glu Lys	Lys Asp Asn Arg Ala	Tyr		
	740	745	750		
Asn Cys Arg Glu	Ala Glu Ser Thr Tyr	Arg Gln Gln Pro Lys	Arg		
	755	760	765		
Pro Gln Lys His	Ile Gln Lys Ala Asp	Ile His Leu Val Pro	Val		
	770	775	780		

Leu Arg Gly Gln	Ala Gly Glu Pro Cys	Glu Val Gly Gln Ser His
785	790	795
Lys Asp Val Asp	Lys Glu Ala Met Met	Glu Ala Gly Trp Asp Pro
800	805	810
Cys Leu Gln Ala	Pro Phe His Leu Thr	Pro Thr Leu Tyr Arg Thr
815	820	825
Leu Arg Asn Gln	Gly Asn Gln Gly Ala	Pro Ala Glu Ser Arg Glu
830	835	840
Val Leu Gln Asp	Thr Val Asn Leu Leu	Phe Asn His Pro Arg Gln
845	850	855
Arg Asn Ala Ser	Arg Glu Asn Leu Asn	Leu Pro Glu Pro Gln Pro
860	865	870
Ala Thr Gly Gln	Pro Arg Ser Arg Pro	Leu Lys Val Ala Gly Ser
875	880	885
Pro Thr Gly Arg	Leu Ala Gly Asp Gln	Gly Ser Glu Glu Ala Pro
890	895	900
Gln Arg Pro Pro	Ala Ser Ser Ala Thr	Leu Arg Arg Gln Arg His
905	910	915
Leu Asn Gly Lys	Val Ser Pro Glu Lys	Glu Ser Gly Pro Arg Gln
920	925	930
Ile Leu Arg Ser	Leu Val Arg Leu Ser	Val Ala Ala Phe Ala Glu
935	940	945
Arg Asn Pro Val	Glu Glu Leu Thr Val	Asp Ser Pro Pro Val Gln
950	955	960
Gln Ile Ser Gln	Leu Leu Ser Leu Leu	His Gln Gly Gln Phe Gln
965	970	975
Pro Lys Pro Asn	His Arg Gly Asn Lys	Tyr Leu Ala Lys Pro Gly
980	985	990
Gly Ser Arg Ser	Ala Ile Pro Asp Thr	Asp Gly Pro Ser Ala Arg
995	1000	1005
Ala Gly Gly Gln	Thr Asp Pro Glu Gln	Glu Glu Gly Pro Leu Asp
1010	1015	1020
Pro Glu Glu Asp	Leu Ser Val Lys Gln	Leu Leu Glu Glu Glu Leu
1025	1030	1035
Ser Ser Leu Leu	Asp Pro Ser Thr Gly	Leu Ala Leu Asp Arg Leu
1040	1045	1050
Ser Ala Pro Asp	Pro Ala Trp Met Ala	Arg Leu Ser Leu Pro Leu
1055	1060	1065
Thr Thr Asn Tyr	Arg Asp Asn Val Ile	Ser Pro Asp Ala Ala Ala

1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala		
1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val		
1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser		
1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser		
1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala		
1145	1150	1155
Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr		
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Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Arg Cys Leu		
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<210> 426

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

gtaagcacat gcctccagag gtgc 24

<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 427

gtgacgtgga tgcttgggat gttg 24

<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

tggacacctt cagtattgat gccaaagacag gccagggtcat tctgcgtcga 50

<210> 429

<211> 2037

<212> DNA
<213> Homo sapiens

<400> 429

cggaacgcgtg ggcgggacgcg tgggggagag ccgcagtccc ggctgcagca 50
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ggcctcgggg agtgggaagt ggaggcagga gccttcctta cacttcgcca 150
tgagtttctt catcgactcc agcatcatga ttacctcca gatactatgt 200
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tttgccctga gattgactca ttaaaatcag agactgtaac aaaaaaaaaa 1950
aaaaaaaaaa agggcgggcg cgactctaga gtcgacctgc agaagcttgg 2000
ccgccatggc ccaacttggt tattgcagct tataatg 2037

<210> 430
<211> 455
<212> PRT
<213> Homo sapiens

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Lys Asp Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser
35 40 45
Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe
50 55 60
Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp
65 70 75
Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val
80 85 90
Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu
95 100 105
His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe
110 115 120

Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser	
				125					130					135	
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val	
				140					145					150	
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly	
				155					160					165	
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn	
				170					175					180	
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln	
				185					190					195	
Thr	Met	Asp	Met	Ile	Ile	Ser	Lys	Lys	Lys	Arg	Met	Ala	Met	Ala	
				200					205					210	
Arg	Arg	Thr	Met	Phe	Gln	Lys	Gly	Glu	Val	His	Asn	Lys	Pro	Ser	
				215					220					225	
Gly	Phe	Trp	Gly	Met	Ile	Lys	Ser	Val	Thr	Thr	Ser	Ala	Ser	Gly	
				230					235					240	
Ser	Glu	Asn	Leu	Thr	Leu	Ile	Gln	Gln	Glu	Val	Asp	Ala	Leu	Glu	
				245					250					255	
Glu	Leu	Ser	Arg	Gln	Leu	Phe	Leu	Glu	Thr	Ala	Asp	Leu	Tyr	Ala	
				260					265					270	
Thr	Lys	Glu	Arg	Ile	Glu	Tyr	Ser	Lys	Thr	Phe	Lys	Gly	Lys	Tyr	
				275					280					285	
Phe	Asn	Phe	Leu	Gly	Tyr	Phe	Phe	Ser	Ile	Tyr	Cys	Val	Trp	Lys	
				290					295					300	
Ile	Phe	Met	Ala	Thr	Ile	Asn	Ile	Val	Phe	Asp	Arg	Val	Gly	Lys	
				305					310					315	
Thr	Asp	Pro	Val	Thr	Arg	Gly	Ile	Glu	Ile	Thr	Val	Asn	Tyr	Leu	
				320					325					330	
Gly	Ile	Gln	Phe	Asp	Val	Lys	Phe	Trp	Ser	Gln	His	Ile	Ser	Phe	
				335					340					345	
Ile	Leu	Val	Gly	Ile	Ile	Ile	Val	Thr	Ser	Ile	Arg	Gly	Leu	Leu	
				350					355					360	
Ile	Thr	Leu	Thr	Lys	Phe	Phe	Tyr	Ala	Ile	Ser	Ser	Ser	Lys	Ser	
				365					370					375	
Ser	Asn	Val	Ile	Val	Leu	Leu	Leu	Ala	Gln	Ile	Met	Gly	Met	Tyr	
				380					385					390	
Phe	Val	Ser	Ser	Val	Leu	Leu	Ile	Arg	Met	Ser	Met	Pro	Leu	Glu	
				395					400					405	
Tyr	Arg	Thr	Ile	Ile	Thr	Glu	Val	Leu	Gly	Glu	Leu	Gln	Phe	Asn	

410	415	420
Phe Tyr His Arg Trp Phe Asp Val Ile	Phe Leu Val Ser Ala Leu	
425	430	435
Ser Ser Ile Leu Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro Glu	
440	445	450
Lys Gln Met Ala Pro		
455		

<210> 431
 <211> 407
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 78, 81, 113, 157, 224, 297
 <223> unknown base

<400> 431
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 tcgactccag catcatgatt acctcccnga nactatTTTT tggatttggg 100
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 <211> 457
 <212> DNA
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<220>
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 <222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
 <223> unknown base

<400> 432
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 ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgtttg 200

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 tctgctgac ctggttttca tggcgcttt ttacattggc tattttattg 350
 tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400
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<220>
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<210> 435
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<211> 1141
<212> PRT
<213> Homo sapiens

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35 40 45
Gly Glu Pro Gly Ser Leu Phe Gly Phe Ser Val Ala Leu His Arg
50 55 60
Gln Leu Gln Pro Arg Pro Gln Ser Trp Leu Leu Val Gly Ala Pro
65 70 75
Gln Ala Leu Ala Leu Pro Gly Gln Gln Ala Asn Arg Thr Gly Gly

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Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg					
				95					100					105					
Val	Asp	Ile	Asp	Gln	Gly	Ala	Asp	Met	Gln	Lys	Glu	Ser	Lys	Glu					
				110					115					120					
Asn	Gln	Trp	Leu	Gly	Val	Ser	Val	Arg	Ser	Gln	Gly	Pro	Gly	Gly					
				125					130					135					
Lys	Ile	Val	Thr	Cys	Ala	His	Arg	Tyr	Glu	Ala	Arg	Gln	Arg	Val					
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Asp	Gln	Ile	Leu	Glu	Thr	Arg	Asp	Met	Ile	Gly	Arg	Cys	Phe	Val					
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Leu	Ser	Gln	Asp	Leu	Ala	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Gly	Glu					
				170					175					180					
Trp	Lys	Phe	Cys	Glu	Gly	Arg	Pro	Gln	Gly	His	Glu	Gln	Phe	Gly					
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Phe	Cys	Gln	Gln	Gly	Thr	Ala	Ala	Ala	Phe	Ser	Pro	Asp	Ser	His					
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Tyr	Leu	Leu	Phe	Gly	Ala	Pro	Gly	Thr	Tyr	Asn	Trp	Lys	Gly	Thr					
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Ala	Arg	Val	Glu	Leu	Cys	Ala	Gln	Gly	Ser	Ala	Asp	Leu	Ala	His					
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Leu	Asp	Asp	Gly	Pro	Tyr	Glu	Ala	Gly	Gly	Glu	Lys	Glu	Gln	Asp					
				245					250					255					
Pro	Arg	Leu	Ile	Pro	Val	Pro	Ala	Asn	Ser	Tyr	Phe	Gly	Phe	Ser					
				260					265					270					
Ile	Asp	Ser	Gly	Lys	Gly	Leu	Val	Arg	Ala	Glu	Glu	Leu	Ser	Phe					
				275					280					285					
Val	Ala	Gly	Ala	Pro	Arg	Ala	Asn	His	Lys	Gly	Ala	Val	Val	Ile					
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Leu	Arg	Lys	Asp	Ser	Ala	Ser	Arg	Leu	Val	Pro	Glu	Val	Met	Leu					
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Ser	Gly	Glu	Arg	Leu	Thr	Ser	Gly	Phe	Gly	Tyr	Ser	Leu	Ala	Val					
				320					325					330					
Ala	Asp	Leu	Asn	Ser	Asp	Gly	Trp	Pro	Asp	Leu	Ile	Val	Gly	Ala					
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Pro	Tyr	Phe	Phe	Glu	Arg	Gln	Glu	Glu	Leu	Gly	Gly	Ala	Val	Tyr					
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Val	Tyr	Leu	Asn	Gln	Gly	Gly	His	Trp	Ala	Gly	Ile	Ser	Pro	Leu					
				365					370					375					

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Val	Leu	Gly	Asp	Leu	Asn	Gln	Asp	Gly	Phe	Pro	Asp	Ile	Ala	Val	
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Gly	Ala	Pro	Phe	Asp	Gly	Asp	Gly	Lys	Val	Phe	Ile	Tyr	His	Gly	
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Ser	Ser	Leu	Gly	Val	Val	Ala	Lys	Pro	Ser	Gln	Val	Leu	Glu	Gly	
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Glu	Ala	Val	Gly	Ile	Lys	Ser	Phe	Gly	Tyr	Ser	Leu	Ser	Gly	Ser	
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Leu	Asp	Met	Asp	Gly	Asn	Gln	Tyr	Pro	Asp	Leu	Leu	Val	Gly	Ser	
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Leu	Ala	Asp	Thr	Ala	Val	Leu	Phe	Arg	Ala	Arg	Pro	Ile	Leu	His	
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Val	Ser	His	Glu	Val	Ser	Ile	Ala	Pro	Arg	Ser	Ile	Asp	Leu	Glu	
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Gln	Pro	Asn	Cys	Ala	Gly	Gly	His	Ser	Val	Cys	Val	Asp	Leu	Arg	
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Val	Cys	Phe	Ser	Tyr	Ile	Ala	Val	Pro	Ser	Ser	Tyr	Ser	Pro	Thr	
				515					520					525	
Val	Ala	Leu	Asp	Tyr	Val	Leu	Asp	Ala	Asp	Thr	Asp	Arg	Arg	Leu	
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Arg	Gly	Gln	Val	Pro	Arg	Val	Thr	Phe	Leu	Ser	Arg	Asn	Leu	Glu	
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Glu	Pro	Lys	His	Gln	Ala	Ser	Gly	Thr	Val	Trp	Leu	Lys	His	Gln	
				560					565					570	
His	Asp	Arg	Val	Cys	Gly	Asp	Ala	Met	Phe	Gln	Leu	Gln	Glu	Asn	
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Val	Lys	Asp	Lys	Leu	Arg	Ala	Ile	Val	Val	Thr	Leu	Ser	Tyr	Ser	
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Leu	Gln	Thr	Pro	Arg	Leu	Arg	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
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Pro	Pro	Val	Ala	Pro	Ile	Leu	Asn	Ala	His	Gln	Pro	Ser	Thr	Gln	
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Arg	Ala	Glu	Ile	His	Phe	Leu	Lys	Gln	Gly	Cys	Gly	Glu	Asp	Lys	
				635					640					645	
Ile	Cys	Gln	Ser	Asn	Leu	Gln	Leu	Val	His	Ala	Arg	Phe	Cys	Thr	
				650					655					660	
Arg	Val	Ser	Asp	Thr	Glu	Phe	Gln	Pro	Leu	Pro	Met	Asp	Val	Asp	

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Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile	Gly		
	680		685		690
Leu Glu Leu Met	Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln	Pro		
	695		700		705
Gln Ala Asp Gly	Asp Asp Ala His Glu	Ala Gln Leu Leu Val	Met		
	710		715		720
Leu Pro Asp Ser	Leu His Tyr Ser Gly	Val Arg Ala Leu Asp	Pro		
	725		730		735
Ala Glu Lys Pro	Leu Cys Leu Ser Asn	Glu Asn Ala Ser His	Val		
	740		745		750
Glu Cys Glu Leu	Gly Asn Pro Met Lys	Arg Gly Ala Gln Val	Thr		
	755		760		765
Phe Tyr Leu Ile	Leu Ser Thr Ser Gly	Ile Ser Ile Glu Thr	Thr		
	770		775		780
Glu Leu Glu Val	Glu Leu Leu Leu Ala	Thr Ile Ser Glu Gln	Glu		
	785		790		795
Leu His Pro Val	Ser Ala Arg Ala Arg	Val Phe Ile Glu Leu	Pro		
	800		805		810
Leu Ser Ile Ala	Gly Met Ala Ile Pro	Gln Gln Leu Phe Phe	Ser		
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Gly Val Val Arg	Gly Glu Arg Ala Met	Gln Ser Glu Arg Asp	Val		
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Gly Ser Lys Val	Lys Tyr Glu Val Thr	Val Ser Asn Gln Gly	Gln		
	845		850		855
Ser Leu Arg Thr	Leu Gly Ser Ala Phe	Leu Asn Ile Met Trp	Pro		
	860		865		870
His Glu Ile Ala	Asn Gly Lys Trp Leu	Leu Tyr Pro Met Gln	Val		
	875		880		885
Glu Leu Glu Gly	Gly Gln Gly Pro Gly	Gln Lys Gly Leu Cys	Ser		
	890		895		900
Pro Arg Pro Asn	Ile Leu His Leu Asp	Val Asp Ser Arg Asp	Arg		
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Arg Arg Arg Glu	Leu Glu Pro Pro Glu	Gln Gln Glu Pro Gly	Glu		
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Arg Gln Glu Pro	Ser Met Ser Trp Trp	Pro Val Ser Ser Ala	Glu		
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Lys Lys Lys Asn	Ile Thr Leu Asp Cys	Ala Arg Gly Thr Ala	Asn		
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Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala
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 Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu
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 Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn
 995 1000 1005
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 1010 1015 1020
 Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val
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 Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro
 1070 1075 1080
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 1085 1090 1095
 Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

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<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 439
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<210> 440

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

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aaaaaaaaaa aaaa 1964

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<212> PRT
<213> Homo sapiens

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35 40 45
Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys

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Cys	Val	Asp	Arg	Tyr	Gly	Asn	Glu	Val	Met	Gly	Ser	Arg	Ile	Asn
				365					370					375
Gly	Val	Ala	Asp	Cys	Ala	Ile	Asp	Phe	Glu	Ile	Ser	Gly	Asp	Phe
				380					385					390
Ala	Ser	Gly	Asp	Phe	His	Glu	Trp	Thr	Asp	Asp	Glu	Asp	Asp	Glu
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Asp	Asp	Ile	Met	Asn	Asp	Glu	Asp	Glu	Ile	Glu	Asp	Asp	Asp	Glu
				410					415					420
Asp	Glu	Gly	Asp	Asp	Asp	Gly	Gly	Asp	Asp	His	Asp	Val	Tyr	
				425					430					435

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<210> 443

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 443

cagcaatatt cagaagcggc aaggg 25

<210> 444

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 444

catcatgggc atcaccacca tcatcatc 28

<210> 445

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 445

ggttactaca agccaacaca atgtcatggc agtggttgac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

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gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350
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tctgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500
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tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctggt 700
ctatggttaa tttagtggc atggtgggtg tgtcagccat tcaagtttat 750
atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaactc 800
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<210> 447
 <211> 229
 <212> PRT
 <213> Homo sapiens

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 20 25 30
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 35 40 45
 Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile
 50 55 60
 Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His
 65 70 75
 Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys
 80 85 90
 Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met
 95 100 105
 Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile

	110		115		120
Phe Phe Glu Leu	Ile Leu Asp Asn Met	Gly Glu Gln Ala Gln Glu			
	125		130		135
Gln Glu Asp Trp	Lys Lys Tyr Ile Thr	Gly Thr Asp Ile Leu Asp			
	140		145		150
Met Lys Leu Glu	Asp Ile Leu Glu Ser	Ile Asn Ser Ile Lys Ser			
	155		160		165
Arg Leu Ser Lys	Ser Gly His Ile Gln	Ile Leu Leu Arg Ala Phe			
	170		175		180
Glu Ala Arg Asp	Arg Asn Ile Gln Glu	Ser Asn Phe Asp Arg Val			
	185		190		195
Asn Phe Trp Ser	Met Val Asn Leu Val	Val Met Val Val Val Ser			
	200		205		210
Ala Ile Gln Val	Tyr Met Leu Lys Ser	Leu Phe Glu Asp Lys Arg			
	215		220		225
Lys Ser Arg Thr					

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 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 448
 cccagcaggg ctgggcgaca aga 23

<210> 449
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 449
 gtcttccagt ttcatatcca ata 23

<210> 450
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 450
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<210> 451
 <211> 859
 <212> DNA
 <213> Homo sapiens

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 gccctgcccc gtgtgtcctg gatgctgctt tcctgcctca ttctcctgtg 150
 tcaggttcaa ggtgaagaaa cccagaagga actgccctct ccacggatca 200
 gctgtcccaa aggctccaag gcctatggct cccctgcta tgccttggtt 250
 ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300
 ctctggaaaa ctggtgtctg tgctcagtgg ggctgagga tccttcgtgt 350
 cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400
 ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450
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 aaaaaaaaaa 859

<210> 452
 <211> 175
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys
 35 40 45
 Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser

	50		55		60
Trp Met Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys	65		70		75
Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val Ser Ser	80		85		90
Leu Val Arg Ser Ile Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly	95		100		105
Leu His Asp Pro Thr Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp	110		115		120
Glu Trp Ser Ser Thr Asp Val Met Asn Tyr Phe Ala Trp Glu Lys	125		130		135
Asn Pro Ser Thr Ile Leu Asn Pro Gly His Cys Gly Ser Leu Ser	140		145		150
Arg Ser Thr Gly Phe Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala	155		160		165
Lys Leu Pro Tyr Val Cys Lys Phe Lys Asp	170		175		

<210> 453
 <211> 550
 <212> DNA
 <213> Homo sapiens

<400> 453
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 ggcgtccttg gcgctgggtgc tggctgcctg cggagagctg gcgccggccc 150
 tgcgtgtgta cgtctgtccg gagcccacag gagtgtcgga ctgtgtcacc 200
 atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250
 ccgggagata gtgtaccctt tccaggggga ctccacggtg accaagtcct 300
 gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350
 cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccgc 400
 tctgaacagc ctccactgog gggccctcac gctcctccca ctcttgagcc 450
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<210> 454
 <211> 125
 <212> PRT
 <213> Homo sapiens

[illegible]

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<210> 455
<211> 1518
<212> DNA
<213> Homo sapiens
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attttctctt	tctttctccc	tcttgagtcc	ttctgagatg	atggctctgg	150
gcgcagcggg	agctaccocg	gtctttgtcg	cgatggtagc	ggcggctctc	200
ggcggccacc	ctctgctggg	agtgagcgcc	accttgaact	cggttctcaa	250
ttccaacgct	atcaagaacc	tgccccacc	gctgggcggc	gctgcggggc	300
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aataagtagc	agaccattga	caactaccag	ccgtaccocg	gcgcagagga	400
cgaggagtgc	ggcactgatg	agtactgcgc	tagtcccacc	cgcgaggagg	450
acgcaggcgt	gcaaattctgt	ctcgccctga	ggaagcgccg	aaaacgctgc	500
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tgtgtcttct	gatcaaaaac	atttccgagg	agaaattgag	gaaaccatca	600

ctgaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650
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 ctgtggagaa ggtctgtctt gccggatata gaaagatcac catcaagcca 900
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 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450
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 catttaaaaa aaaaaaaaa 1518

<210> 456
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 456
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 20 25 30
 Ala Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu
 35 40 45
 Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val
 50 55 60
 Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln
 65 70 75

Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	
				80					85					90	
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	
				95					100					105	
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	
				110					115					120	
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	
				125					130					135	
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	
				140					145					150	
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	
				155					160					165	
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	
				170					175					180	
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	
				185					190					195	
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	
				200					205					210	
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	
				215					220					225	
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	
				230					235					240	
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	
				245					250					255	
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<210> 457

<211> 638

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473, 509, 556

<223> unknown base

<400> 457

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 <211> 4040
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 ttctctcctg cacgcggtgc ttgggctcgg ccaggcgggg tccgccgcca 150
 gggtttgagg atgggggagt agctacagga agcgaccccc cgatggcaag 200
 gtatatTTTT gtggaatgaa aaggaaagtat tagaaatgag ctgaagacca 250
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tagagttcta tattttaaag atatatgtgt tcatgtattt tctgaaattg 3550
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attattcaaa taggaaaaat tactttacag gttgttttac tgtagcttat 3750

	200	205	210
Met Ala Pro Val	Lys Tyr His Gly Asp	Arg Ser Lys Glu Ser	Leu
	215	220	225
Val Ser Phe Ala	Met Gln His Val Arg	Ser Thr Val Thr Glu	Leu
	230	235	240
Trp Thr Gly Asn	Phe Val Asn Ser Ile	Gln Thr Ala Phe Ala	Ala
	245	250	255
Gly Ile Gly Trp	Leu Ile Thr Phe Cys	Ser Lys Gly Gly Asp	Cys
	260	265	270
Leu Thr Ser Gln	Thr Arg Leu Arg Leu	Ser Gly Met Leu Phe	Leu
	275	280	285
Asn Ser Leu Asp	Ala Lys Glu Ile Tyr	Leu Glu Val Ile His	Asn
	290	295	300
Leu Pro Asp Phe	Glu Leu Leu Ser Ala	Asn Thr Leu Glu Asp	Arg
	305	310	315
Leu Ala His His	Arg Trp Leu Leu Phe	Phe His Phe Gly Lys	Asn
	320	325	330
Glu Asn Ser Asn	Asp Pro Glu Leu Lys	Lys Leu Lys Thr Leu	Leu
	335	340	345
Lys Asn Asp His	Ile Gln Val Gly Arg	Phe Asp Cys Ser Ser	Ala
	350	355	360
Pro Asp Ile Cys	Ser Asn Leu Tyr Val	Phe Gln Pro Ser Leu	Ala
	365	370	375
Val Phe Lys Gly	Gln Gly Thr Lys Glu	Tyr Glu Ile His His	Gly
	380	385	390
Lys Lys Ile Leu	Tyr Asp Ile Leu Ala	Phe Ala Lys Glu Ser	Val
	395	400	405
Asn Ser His Val	Thr Thr Leu Gly Pro	Gln Asn Phe Pro Ala	Asn
	410	415	420
Asp Lys Glu Pro	Trp Leu Val Asp Phe	Phe Ala Pro Trp Cys	Pro
	425	430	435
Pro Cys Arg Ala	Leu Leu Pro Glu Leu	Arg Arg Ala Ser Asn	Leu
	440	445	450
Leu Tyr Gly Gln	Leu Lys Phe Gly Thr	Leu Asp Cys Thr Val	His
	455	460	465
Glu Gly Leu Cys	Asn Met Tyr Asn Ile	Gln Ala Tyr Pro Thr	Thr
	470	475	480
Val Val Phe Asn	Gln Ser Asn Ile His	Glu Tyr Glu Gly His	His
	485	490	495

Ser	Ala	Glu	Gln	Ile	Leu	Glu	Phe	Ile	Glu	Asp	Leu	Met	Asn	Pro	
				500					505					510	
Ser	Val	Val	Ser	Leu	Thr	Pro	Thr	Thr	Phe	Asn	Glu	Leu	Val	Thr	
				515					520					525	
Gln	Arg	Lys	His	Asn	Glu	Val	Trp	Met	Val	Asp	Phe	Tyr	Ser	Pro	
				530					535					540	
Trp	Cys	His	Pro	Cys	Gln	Val	Leu	Met	Pro	Glu	Trp	Lys	Arg	Met	
				545					550					555	
Ala	Arg	Thr	Leu	Thr	Gly	Leu	Ile	Asn	Val	Gly	Ser	Ile	Asp	Cys	
				560					565					570	
Gln	Gln	Tyr	His	Ser	Phe	Cys	Ala	Gln	Glu	Asn	Val	Gln	Arg	Tyr	
				575					580					585	
Pro	Glu	Ile	Arg	Phe	Phe	Pro	Pro	Lys	Ser	Asn	Lys	Ala	Tyr	Gln	
				590					595					600	
Tyr	His	Ser	Tyr	Asn	Gly	Trp	Asn	Arg	Asp	Ala	Tyr	Ser	Leu	Arg	
				605					610					615	
Ile	Trp	Gly	Leu	Gly	Phe	Leu	Pro	Gln	Val	Ser	Thr	Asp	Leu	Thr	
				620					625					630	
Pro	Gln	Thr	Phe	Ser	Glu	Lys	Val	Leu	Gln	Gly	Lys	Asn	His	Trp	
				635					640					645	
Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe	
				650					655					660	
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val	
				665					670					675	
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln	
				680					685					690	
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr	
				695					700					705	
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg	
				710					715					720	
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr	
				725					730					735	
Leu	Arg	Asn	Gln	Gly	Lys	Arg	Asn	Lys	Asp	Glu	Leu				
				740					745						

<210> 460

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460
actccccagg ctgttcacac tgcc 24

<210> 461

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461

gatcagccag ccaataccag cagc 24

<210> 462

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 462

gtggtgatga tagaatgctt tgccgaatga aaggagtcaa cagctatccc 50

<210> 463

<211> 1818

<212> DNA

<213> Homo sapiens

<400> 463

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ggacagagca aagccatgaa catcatccta gaaatccttc tgcttctgat 100

caccatcatc tactcctact tggagtcgtt ggtgaagttt ttcattcctc 150

agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200

catggaatag gcaggcagac tacttatgaa tttgcaaaac gacagagcat 250

attggttctg tgggatatta ataagcgcgg tgtggaggaa actgcagctg 300

agtgccgaaa actaggcgtc actgcgcgtg cgtatgtggt agactgcagc 350

aacagagaag agatctatcg ctctctaaat caggatgaaga aagaagtggg 400

tgatgtaaca atcgtggtga ataatgctgg gacagtatat ccagccgatc 450

ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500

ctaggacatt tttggatcac aaaagcactt cttccatcga tgatggagag 550

aaatcatggc cacatcgtca cagtggcttc agtgtgcggc cacgaaggga 600

ttccttacct catcccatat tgttccagca aatttgccgc tgttggcttt 650

cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700

aacctcatgt ctctgccag tttttgtgaa tactgggttc accaaaaatc 750
 caagcacaag attatggcct gtattggaga cagatgaagt cgtaagaagt 800
 ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta 850
 tatcaatatc tttctgagac tacagaagtt tcttcctgaa cgcgcctcag 900
 cgatttttaa tcgtatgcag aatattcaat ttgaagcagt ggttggccac 950
 aaaatcaaaa tgaaatgaat aaataagctc cagccagaga tgtatgcatg 1000
 ataatgatat gaatagtttc gaatcaatgc tgcaaagctt tatttcacat 1050
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 tagccatgcc acagaatatc aacaagaaca cagaatgagt gcacagctaa 1400
 gagatcaagt ttcagcaggc agctttatct caacctggac atattttaag 1450
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 gaattttaag ttctagcccc atgataacct ttttctttgt aatttatgct 1700
 ttcatatatc cttggtccca gagatgttta gacaatttta ggctcaaaaa 1750
 ttaaagctaa cacaggaaaa ggaactgtac tggctattac ataagaaaca 1800
 atggacccaa gagaagaa 1818

<210> 464
 <211> 300
 <212> PRT
 <213> Homo sapiens

<400> 464
 Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile
 1 5 10 15
 Tyr Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg
 20 25 30

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atcgatattg ttttttaaga ttaatatatt tcaggtatatt aatacga 1547

<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met Thr Lys Ala Arg Leu Phe Arg Leu Trp Leu Val Leu Gly Ser
1 5 10 15

Val Phe Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly
20 25 30

Ala Ala His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr
35 40 45

Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu
50 55 60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser
65 70 75

Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln
80 85 90

Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp
95 100 105

Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln
110 115 120

Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser
125 130 135

Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro
140 145 150

Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala
155 160 165

Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg
170 175 180

Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro
185 190 195

Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala
200 205 210

Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys
215 220 225

Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys
230 235 240

Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe	
				245					250					255	
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe	
				260					265					270	
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro	
				275					280					285	
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe	
				290					295					300	
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu	
				305					310					315	
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His	
				320					325					330	
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu	
				335					340					345	
Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg	
				350					355					360	
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser	
				365					370					375	
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln	
				380					385					390	
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr	
				395					400					405	
Pro	Lys	Pro	Glu	Asn	Leu	Leu	Arg	Asp							
				410											

<210> 467
 <211> 1071
 <212> DNA
 <213> Homo sapiens

<400> 467
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 acgggatggc tacgggaacg cgctatgccg ggaaggtggt ggtcgtgacc 150
 gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200
 cggggcccca gtggttatct gcgacaagga tgagtctggg ggccggggccc 250
 tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300
 gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttggccg 350
 cctggattgt gttgtcaaca acgctggcca ccaccaccc ccacagaggc 400

ctgaggagac ctctgccag ggattccgcc agctgctgga gctgaaccta 450
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 tcaagggaat gtcacaaaca tctccagcct ggtgggggca atcgccagag 550
 cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600
 aaagcttttg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650
 ctccccagga aacatctgga ccccgctgtg ggaggagctg gcagccttaa 700
 tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750
 gggcgcatgg gccagcccg ctaggtcggg gctgcggcag tgttcctggc 800
 ctccgaagcc aacttctgca cgggcattga actgctcgtg acggggggtg 850
 cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900
 cccgatatcc cttcctgatt tctctcattt ctacttgggg ccccttct 950
 aggactctcc caccctaaac tccaacctgt atcagatgca gcccccaagc 1000
 ccttagactc taagcccagt tagcaagggtg ccgggtcacc ctgcagggtc 1050
 ccataaaaac gatttcagc c 1071

<210> 468
 <211> 270
 <212> PRT
 <213> Homo sapiens

<400> 468
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 20 25 30
 Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly
 35 40 45
 Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu
 50 55 60
 Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu
 65 70 75
 Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala
 80 85 90
 Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln
 95 100 105
 Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr
 110 115 120

Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr	Leu	Arg	Lys	Ser	Gln	Gly	Asn	
				125					130					135	
Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly	Ala	Ile	Gly	Gln	Ala	Gln	
				140					145					150	
Ala	Val	Pro	Tyr	Val	Ala	Thr	Lys	Gly	Ala	Val	Thr	Ala	Met	Thr	
				155					160					165	
Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly	Val	Arg	Val	Asn	
				170					175					180	
Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp	Glu	Glu	Leu	
				185					190					195	
Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu	Gly	Met	
				200					205					210	
Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly	
				215					220					225	
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly	
				230					235					240	
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys	
				245					250					255	
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser	
				260					265					270	

<210> 469
 <211> 687
 <212> DNA
 <213> Homo sapiens

<400> 469
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 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100
 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200
 aaaccgtatg ccgcgatgga ggagtatgag aggaacatcg aggagatggt 250
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgaggtca 300
 acttgcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400
 gtgccttgtg ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450
 gcatggtgag cgtgccggtg ttcagccagg ttcctgtgcg ccgccgcctc 500
 tgcccgccac cgccccgcac agggccttgc cgccagcgcg cagtcattgga 550

gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600
gccaggccag cagcccgaga ccacccctct tgcacctttg tgccaagaaa 650
ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470
<211> 180
<212> PRT
<213> Homo sapiens

<400> 470
Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile
1 5 10 15
Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
20 25 30
Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val
35 40 45
Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu
50 55 60
Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn
65 70 75
Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu
80 85 90
Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile
95 100 105
Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg
110 115 120
Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp
125 130 135
Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
140 145 150
Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln
155 160 165
Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
170 175 180

<210> 471
<211> 2368
<212> DNA
<213> Homo sapiens

<400> 471
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aaacccggcg ggcgagcgag gctgcgggcc ggccgctgcc cttccccaca 100

ctccccgccg agaagcctcg ctcgggcgccc aacatggcgg gtgggcgctg 150
cggccccgag ctaacggcgc tcctggccgc ctggatcgcg gctgtggcgg 200
cgacggcagg ccccgaggag gccgcgctgc cgccggagca gagccgggtc 250
cagcccatga ccgcctccaa ctggacgctg gtgatggagg gcgagtggat 300
gctgaaatth tacgccccat ggtgtccatc ctgccagcag actgattcag 350
aatgggaggc ttttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400
aaggtagatg tcattcaaga accaggthtg agtggccgct tctttgtcac 450
cactctccca gcathththc atgcaaagga tgggatattc cgccgttatc 500
gtggcccagg aatcttcgaa gacctgcaga attatatctt agagaagaaa 550
tggcaatcag tcgagcctct gactggctgg aaatccccag cttctctaac 600
gatgtctgga atggctggtc tththtagcat ctctggcaag atatggcatc 650
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gtgtththtcg tcatagccac cttggththth ggctththta tgggtctggt 750
cttggtggtg atatcagaat gththctatgt gccacttcca aggcatthtat 800
ctgagcgttc tgagcagaat cggagatcag aggaggctca tagagctgaa 850
cagttgcagg atgcggagga ggaaaaagat gattcaaathg aagaagaaaa 900
caaagacagc cttgtagatg atgaagaaga gaaagaagat cttggcgatg 950
aggatgaagc agaggaagaa gaggaggagg acaacttggc tgctggtgtg 1000
gatgaggaga gaagtgaggc caatgatcag gggccccag gagaggacgg 1050
tgtgacccgg gaggaagtag agcctgagga ggctgaagaa ggcatctctg 1100
agcaaccctg ccagctgac acagaggthg tggaagactc cttgaggcag 1150
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caagaataca caccaaaaaca atatgtcagc thccctthtg cctgcagthth 1250
gtaccaaatc cthaththth cctgaatgag caagctthth ttaaaagatg 1300
ctctctagtc atthggtctc atggcagtaa gcctcatgta tactaaggag 1350
agtctthccag gtgtgacaat caggatatag aaaaacaaac gtagtgthtg 1400
gatctgthth gagactggga tgggaacaag thcaththact taggggtcag 1450
agagtctcga ccagaggagg ccaththccag thctaathcag cacctthccag 1500
agacaaggct gcaggccctg tgaaatgaaa gccaaagcagg agcctthggt 1550

cctgagcatc cccaaagtgt aacgtagaag ccttgcatcc ttttcttgtg 1600
 taaagtatth atthttgtca aattgcagga aacatcaggc accacagtgc 1650
 atgaaaaatc tttcacagct agaaattgaa agggccttgg gtatagagag 1700
 cagctcagaa gtcacccag ccctctgaat ctctgtgtgt atgttttatt 1750
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 acactcttca ctattatctc ttggtcagag gactccaata acagccaggt 1850
 ttacatgaac tgtgtttgtt cattctgacc taaggggttt agataatcag 1900
 taaccataac ccctgaagct gtgactgcc aacatctcaa atgaaatgtt 1950
 gtggccatca gagactcaaa aggaagtaag gatttttaca gacagattaa 2000
 aaaaaaattg ttttgtccaa aatatagttg ttgttgattt ttttttaagt 2050
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 acctgaaagt gaaagatttg atthtgtttc catcttctgt aatcttccaa 2300
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<210> 472
 <211> 349
 <212> PRT
 <213> Homo sapiens

<400> 472
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 Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser
 35 40 45
 Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr
 50 55 60
 Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu
 65 70 75
 Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys
 80 85 90

Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val	95	100	105
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg	110	115	120
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile	125	130	135
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys	140	145	150
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser	155	160	165
Ile	Ser	Gly	Lys	Ile	Trp	His	Leu	His	Asn	Tyr	Phe	Thr	Val	Thr	170	175	180
Leu	Gly	Ile	Pro	Ala	Trp	Cys	Ser	Tyr	Val	Phe	Phe	Val	Ile	Ala	185	190	195
Thr	Leu	Val	Phe	Gly	Leu	Phe	Met	Gly	Leu	Val	Leu	Val	Val	Ile	200	205	210
Ser	Glu	Cys	Phe	Tyr	Val	Pro	Leu	Pro	Arg	His	Leu	Ser	Glu	Arg	215	220	225
Ser	Glu	Gln	Asn	Arg	Arg	Ser	Glu	Glu	Ala	His	Arg	Ala	Glu	Gln	230	235	240
Leu	Gln	Asp	Ala	Glu	Glu	Glu	Lys	Asp	Asp	Ser	Asn	Glu	Glu	Glu	245	250	255
Asn	Lys	Asp	Ser	Leu	Val	Asp	Asp	Glu	Glu	Glu	Lys	Glu	Asp	Leu	260	265	270
Gly	Asp	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asn	Leu	275	280	285
Ala	Ala	Gly	Val	Asp	Glu	Glu	Arg	Ser	Glu	Ala	Asn	Asp	Gln	Gly	290	295	300
Pro	Pro	Gly	Glu	Asp	Gly	Val	Thr	Arg	Glu	Glu	Val	Glu	Pro	Glu	305	310	315
Glu	Ala	Glu	Glu	Gly	Ile	Ser	Glu	Gln	Pro	Cys	Pro	Ala	Asp	Thr	320	325	330
Glu	Val	Val	Glu	Asp	Ser	Leu	Arg	Gln	Arg	Lys	Ser	Gln	His	Ala	335	340	345
Asp Lys Gly Leu																	

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 473
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<210> 474
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 474
ctctcctcat ccacaccagc agcc 24

<210> 475
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 475
gtggatgctg aaattttacg ccccatggtg tccatcctgc cagc 44

<210> 476
<211> 2478
<212> DNA
<213> Homo sapiens

<400> 476
atctggttga actacttaag cttaatttgt taaactccgg taagtaccta 50
gccacatga ttgactcag agattctctt ttgtccacag acagtcattct 100
caggggcaga aagaaaagag ctcccaaattg ctatatctat tcaggggctc 150
tcaagaacaa tggaatatca tcttgattta gaaaatttgg atgaagatgg 200
atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250
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gtaatttttg gaatcctatg cttggtaata ctggtgatag ctgtggtcct 350
gggtaccatg ggggttcttt ccagcccttg tctcctaata tggattatat 400
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ctcaaatgaa ttgggattta tagtaaaaca agtgtcttcc caacctgata 550
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 gtagtaagga ggacagaaaa cagaacagaa aagagtaaca gctgaggtca 850
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<210> 477

<211> 201

<212> PRT

<213> Homo sapiens

<400> 477

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Thr	Gln	Leu	His	Phe	Asp	Ser	Gln	Ser	Asn	Thr	Arg	Ile	Ala	Val	
				20					25					30	
Val	Ser	Glu	Lys	Gly	Ser	Cys	Ala	Ala	Ser	Pro	Pro	Trp	Arg	Leu	
				35					40					45	
Ile	Ala	Val	Ile	Leu	Gly	Ile	Leu	Cys	Leu	Val	Ile	Leu	Val	Ile	
				50					55					60	
Ala	Val	Val	Leu	Gly	Thr	Met	Gly	Val	Leu	Ser	Ser	Pro	Cys	Pro	
				65					70					75	
Pro	Asn	Trp	Ile	Ile	Tyr	Glu	Lys	Ser	Cys	Tyr	Leu	Phe	Ser	Met	
				80					85					90	
Ser	Leu	Asn	Ser	Trp	Asp	Gly	Ser	Lys	Arg	Gln	Cys	Trp	Gln	Leu	
				95					100					105	
Gly	Ser	Asn	Leu	Leu	Lys	Ile	Asp	Ser	Ser	Asn	Glu	Leu	Gly	Phe	
				110					115					120	
Ile	Val	Lys	Gln	Val	Ser	Ser	Gln	Pro	Asp	Asn	Ser	Phe	Trp	Ile	
				125					130					135	
Gly	Leu	Ser	Arg	Pro	Gln	Thr	Glu	Val	Pro	Trp	Leu	Trp	Glu	Asp	
				140					145					150	
Gly	Ser	Thr	Phe	Ser	Ser	Asn	Leu	Phe	Gln	Ile	Arg	Thr	Thr	Ala	
				155					160					165	
Thr	Gln	Glu	Asn	Pro	Ser	Pro	Asn	Cys	Val	Trp	Ile	His	Val	Ser	

170

175

180

Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys
185 190 195

Glu Lys Lys Phe Ser Met
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<210> 478

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 478

gtccacagac agtcattctca ggagcag 27

<210> 479

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 479

acaagtgtct tcccaacctg 20

<210> 480

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 480

atcctcccag agccatggta cctc 24

<210> 481

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 481

ccaaggatag ctgttggttc agagaaagga tcgtgtgctg catctcctcc 50

t 51

<210> 482

<211> 3819

<212> DNA

<213> Homo sapiens

<400> 482

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tcttggtca tcgtaacctc cacctcccgg gttcaagtga ttctcatgcc 150
tcagcctccc gagtagctgg gattacaggt ggtgacttcc aagagtgact 200
ccgtcggagg aaaatgactc cccagtcgct gctgcagacg aactgttcc 250
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Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe	
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Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	
				95					100					105	
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	
				110					115					120	
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	
				125					130					135	
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	
				140					145					150	
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	
				155					160					165	
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	
				170					175					180	
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	
				185					190					195	
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	
				200					205					210	
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	
				215					220					225	
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	
				230					235					240	
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	
				245					250					255	
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	
				260					265					270	
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	
				275					280					285	
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	
				290					295					300	
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	
				305					310					315	
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	
				320					325					330	
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	
				335					340					345	
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	
				350					355					360	
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	

	365		370		375
Ser Cys Phe Cys	Asn His Leu Thr Tyr	Phe Ala Val Leu Met	Val		
	380	385	390		
Ser Ser Val Glu	Val Asp Ala Val His	Lys His Tyr Leu Ser	Leu		
	395	400	405		
Leu Ser Tyr Val	Gly Cys Val Val Ser	Ala Leu Ala Cys Leu	Val		
	410	415	420		
Thr Ile Ala Ala	Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys	Arg		
	425	430	435		
Arg Lys Pro Arg	Asp Tyr Thr Ile Lys	Val His Met Asn Leu	Leu		
	440	445	450		
Leu Ala Val Phe	Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu	Pro		
	455	460	465		
Val Ala Leu Thr	Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala	Ile		
	470	475	480		
Phe Leu His Phe	Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly	Leu		
	485	490	495		
Glu Gly Tyr Asn	Leu Tyr Arg Leu Val	Val Glu Val Phe Gly	Thr		
	500	505	510		
Tyr Val Pro Gly	Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp	Gly		
	515	520	525		
Phe Pro Ile Phe	Leu Val Thr Leu Val	Ala Leu Val Asp Val	Asp		
	530	535	540		
Asn Tyr Gly Pro	Ile Ile Leu Ala Val	His Arg Thr Pro Glu	Gly		
	545	550	555		
Val Ile Tyr Pro	Ser Met Cys Trp Ile	Arg Asp Ser Leu Val	Ser		
	560	565	570		
Tyr Ile Thr Asn	Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe	Asn		
	575	580	585		
Met Ala Met Leu	Ala Thr Met Val Val	Gln Ile Leu Arg Leu	Arg		
	590	595	600		
Pro His Thr Gln	Lys Trp Ser His Val	Leu Thr Leu Leu Gly	Leu		
	605	610	615		
Ser Leu Val Leu	Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser	Phe		
	620	625	630		
Ala Ser Gly Thr	Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser	Ile		
	635	640	645		
Ile Thr Ser Phe	Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp	Ser		
	650	655	660		

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser
680 685 690

Ser Arg Ile

<210> 484
<211> 516
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 68, 70, 84, 147
<223> unknown base

<400> 484
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cgggtggccct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200
cctgcacttc tctgctcac ctgcctttcc tggatgggcc tcgaggggta 250
caacctctac cgactcgtgg tggaggtctt tggcacctat gtccctggct 300
acctactcaa gctgagcgcc atgggctggg gcttcccat ctttctggtg 350
acgctggtgg cctggtgga tgtggacaac tatggcccca tcatcttggc 400
tgtgcatagg actccagagg gcgtcatcta cccttccatg tgctggatcc 450
gggactccct ggtcagctac atcaccaacc tgggcctctt cagcctggtg 500
tttctgttca acatgg 516

<210> 485
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 485
ggcattggag cagtgctggg tg 22

<210> 486
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 486
tggaggccta gatgcggctg gacg 24

<210> 487
<211> 2849
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2715
<223> unknown base

<400> 487
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<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

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Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln	35	40	45	
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser	50	55	60	
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp	65	70	75	
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe	80	85	90	
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys	95	100	105	
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu	110	115	120	
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser	125	130	135	
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe	140	145	150	
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro	155	160	165	
Gln	Phe	Thr	Glu	Ala	Val	Ser	Pro	Ser	Val	Leu	Pro	Pro	Ser	Ala	170	175	180	
Leu	Pro	Leu	Asp	Leu	Leu	Asn	Asn	Ala	Ile	Thr	Ala	Phe	Ser	Thr	185	190	195	

Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp	Gln	Leu
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Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys
				215					220					225
Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu
				230					235					240
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe
				245					250					255
Ser	Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe
				260					265					270
Trp	Pro	Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala
				275					280					285
Cys	Cys	Leu	His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys
				290					295					300
Val	Thr	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr
				305					310					315
Gly	Val	Arg	Gly	Leu	His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu
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His	His	Glu	Glu	Cys	Asp	Cys	Val	Cys	Arg	Gly	Ser	Thr	Gly	Gly
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

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<212> DNA

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<223> Synthetic oligonucleotide probe

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<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491

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<223> Synthetic oligonucleotide probe

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<210> 495

<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

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ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150

aaactccttg gggctagatg gtttcctaaa actctgccct gtgatgtcac 200

tctggatggt ccaaagaacc atgtgatcgt ggactgcaca gacaagcatt 250

tgacagaaat tcctggaggt attcccacga acaccacgaa cctcaccctc 300

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ccatctggta gagatcgatt tcagatgcaa ctgtgtacct attccactgg 400
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<211> 1049

<213> Homo sapiens

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Phe Asn Ile Ile Leu Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe
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Pro Lys Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn
35 40 45

His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro
50 55 60

Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn
65 70 75

His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His
80 85 90

Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu
95 100 105

Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro
110 115 120

Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp
125 130 135

Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu
140 145 150

Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys
155 160 165

Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly
170 175 180

Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile
185 190 195

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser
200 205 210

Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser
215 220 225

Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile
230 235 240

Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp
245 250 255

Leu	Ser	Gly	Asn	Cys	Pro	Arg	Cys	Tyr	Asn	Ala	Pro	Phe	Pro	Cys	
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Ala	Pro	Cys	Lys	Asn	Asn	Ser	Pro	Leu	Gln	Ile	Pro	Val	Asn	Ala	
				275					280					285	
Phe	Asp	Ala	Leu	Thr	Glu	Leu	Lys	Val	Leu	Arg	Leu	His	Ser	Asn	
				290					295					300	
Ser	Leu	Gln	His	Val	Pro	Pro	Arg	Trp	Phe	Lys	Asn	Ile	Asn	Lys	
				305					310					315	
Leu	Gln	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Phe	Leu	Ala	Lys	Glu	Ile	
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Gly	Asp	Ala	Lys	Phe	Leu	His	Phe	Leu	Pro	Ser	Leu	Ile	Gln	Leu	
				335					340					345	
Asp	Leu	Ser	Phe	Asn	Phe	Glu	Leu	Gln	Val	Tyr	Arg	Ala	Ser	Met	
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Asn	Leu	Ser	Gln	Ala	Phe	Ser	Ser	Leu	Lys	Ser	Leu	Lys	Ile	Leu	
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Arg	Ile	Arg	Gly	Tyr	Val	Phe	Lys	Glu	Leu	Lys	Ser	Phe	Asn	Leu	
				380					385					390	
Ser	Pro	Leu	His	Asn	Leu	Gln	Asn	Leu	Glu	Val	Leu	Asp	Leu	Gly	
				395					400					405	
Thr	Asn	Phe	Ile	Lys	Ile	Ala	Asn	Leu	Ser	Met	Phe	Lys	Gln	Phe	
				410					415					420	
Lys	Arg	Leu	Lys	Val	Ile	Asp	Leu	Ser	Val	Asn	Lys	Ile	Ser	Pro	
				425					430					435	
Ser	Gly	Asp	Ser	Ser	Glu	Val	Gly	Phe	Cys	Ser	Asn	Ala	Arg	Thr	
				440					445					450	
Ser	Val	Glu	Ser	Tyr	Glu	Pro	Gln	Val	Leu	Glu	Gln	Leu	His	Tyr	
				455					460					465	
Phe	Arg	Tyr	Asp	Lys	Tyr	Ala	Arg	Ser	Cys	Arg	Phe	Lys	Asn	Lys	
				470					475					480	
Glu	Ala	Ser	Phe	Met	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	
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Gln	Thr	Leu	Asp	Leu	Ser	Lys	Asn	Ser	Ile	Phe	Phe	Val	Lys	Ser	
				500					505					510	
Ser	Asp	Phe	Gln	His	Leu	Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	
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Gly	Asn	Leu	Ile	Ser	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	
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Leu	Ala	Glu	Leu	Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp	

545	550	555
Leu Leu His Ser Thr Ala Phe Glu Glu	Leu His Lys Leu Glu Val	
560	565	570
Leu Asp Ile Ser Ser Asn Ser His Tyr	Phe Gln Ser Glu Gly Ile	
575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn	Leu Lys Val Leu Gln Lys	
590	595	600
Leu Met Met Asn Asp Asn Asp Ile Ser	Ser Ser Thr Ser Arg Thr	
605	610	615
Met Glu Ser Glu Ser Leu Arg Thr Leu	Glu Phe Arg Gly Asn His	
620	625	630
Leu Asp Val Leu Trp Arg Glu Gly Asp	Asn Arg Tyr Leu Gln Leu	
635	640	645
Phe Lys Asn Leu Leu Lys Leu Glu Glu	Leu Asp Ile Ser Lys Asn	
650	655	660
Ser Leu Ser Phe Leu Pro Ser Gly Val	Phe Asp Gly Met Pro Pro	
665	670	675
Asn Leu Lys Asn Leu Ser Leu Ala Lys	Asn Gly Leu Lys Ser Phe	
680	685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys	Asn Leu Glu Thr Leu Asp	
695	700	705
Leu Ser His Asn Gln Leu Thr Thr Val	Pro Glu Arg Leu Ser Asn	
710	715	720
Cys Ser Arg Ser Leu Lys Asn Leu Ile	Leu Lys Asn Asn Gln Ile	
725	730	735
Arg Ser Leu Thr Lys Tyr Phe Leu Gln	Asp Ala Phe Gln Leu Arg	
740	745	750
Tyr Leu Asp Leu Ser Ser Asn Lys Ile	Gln Met Ile Gln Lys Thr	
755	760	765
Ser Phe Pro Glu Asn Val Leu Asn Asn	Leu Lys Met Leu Leu Leu	
770	775	780
His His Asn Arg Phe Leu Cys Thr Cys	Asp Ala Val Trp Phe Val	
785	790	795
Trp Trp Val Asn His Thr Glu Val Thr	Ile Pro Tyr Leu Ala Thr	
800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala	His Lys Gly Gln Ser Val	
815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu	Leu Asp Leu Thr Asn Leu	
830	835	840

Ile	Leu	Phe	Ser	Leu	Ser	Ile	Ser	Val	Ser	Leu	Phe	Leu	Met	Val	
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Met	Met	Thr	Ala	Ser	His	Leu	Tyr	Phe	Trp	Asp	Val	Trp	Tyr	Ile	
				860					865					870	
Tyr	His	Phe	Cys	Lys	Ala	Lys	Ile	Lys	Gly	Tyr	Gln	Arg	Leu	Ile	
				875					880					885	
Ser	Pro	Asp	Cys	Cys	Tyr	Asp	Ala	Phe	Ile	Val	Tyr	Asp	Thr	Lys	
				890					895					900	
Asp	Pro	Ala	Val	Thr	Glu	Trp	Val	Leu	Ala	Glu	Leu	Val	Ala	Lys	
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Arg	Asp	Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu	Ser	Gln	
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Ser	Ile	Gln	Leu	Ser	Lys	Lys	Thr	Val	Phe	Val	Met	Thr	Asp	Lys	
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Tyr	Ala	Lys	Thr	Glu	Asn	Phe	Lys	Ile	Ala	Phe	Tyr	Leu	Ser	His	
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Gln	Arg	Leu	Met	Asp	Glu	Lys	Val	Asp	Val	Ile	Ile	Leu	Ile	Phe	
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Arg	Leu	Cys	Gly	Ser	Ser	Val	Leu	Glu	Trp	Pro	Thr	Asn	Pro	Gln	
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Ala	His	Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Ala	Thr	
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 <211> 4199
 <212> DNA
 <213> Homo sapiens

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 <211> 1041
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr

Val Gly Lys Tyr	Val Thr Glu Leu Asp	Leu Ser Asp Asn Phe Ile
65	70	75
Thr His Ile Thr	Asn Glu Ser Phe Gln Gly	Leu Gln Asn Leu Thr
80	85	90
Lys Ile Asn Leu	Asn His Asn Pro Asn Val	Gln His Gln Asn Gly
95	100	105
Asn Pro Gly Ile	Gln Ser Asn Gly Leu Asn	Ile Thr Asp Gly Ala
110	115	120
Phe Leu Asn Leu	Lys Asn Leu Arg Glu Leu	Leu Leu Glu Asp Asn
125	130	135
Gln Leu Pro Gln	Ile Pro Ser Gly Leu Pro	Glu Ser Leu Thr Glu
140	145	150
Leu Ser Leu Ile	Gln Asn Asn Ile Tyr Asn	Ile Thr Lys Glu Gly
155	160	165
Ile Ser Arg Leu	Ile Asn Leu Lys Asn Leu	Tyr Leu Ala Trp Asn
170	175	180
Cys Tyr Phe Asn	Lys Val Cys Glu Lys Thr	Asn Ile Glu Asp Gly
185	190	195
Val Phe Glu Thr	Leu Thr Asn Leu Glu Leu	Leu Ser Leu Ser Phe
200	205	210
Asn Ser Leu Ser	His Val Pro Pro Lys Leu	Pro Ser Ser Leu Arg
215	220	225
Lys Leu Phe Leu	Ser Asn Thr Gln Ile Lys	Tyr Ile Ser Glu Glu
230	235	240
Asp Phe Lys Gly	Leu Ile Asn Leu Thr Leu	Leu Asp Leu Ser Gly
245	250	255
Asn Cys Pro Arg	Cys Phe Asn Ala Pro Phe	Pro Cys Val Pro Cys
260	265	270
Asp Gly Gly Ala	Ser Ile Asn Ile Asp Arg	Phe Ala Phe Gln Asn
275	280	285
Leu Thr Gln Leu	Arg Tyr Leu Asn Leu Ser	Ser Thr Ser Leu Arg
290	295	300
Lys Ile Asn Ala	Ala Trp Phe Lys Asn Met	Pro His Leu Lys Val
305	310	315
Leu Asp Leu Glu	Phe Asn Tyr Leu Val Gly	Glu Ile Val Ser Gly
320	325	330
Ala Phe Leu Thr	Met Leu Pro Arg Leu Glu	Ile Leu Asp Leu Ser
335	340	345

Phe Asn Tyr Ile	Lys Gly Ser Tyr Pro	Gln His Ile Asn Ile	Ser
350	355	360	
Arg Asn Phe Ser	Lys Leu Leu Ser Leu	Arg Ala Leu His Leu	Arg
365	370	375	
Gly Tyr Val Phe	Gln Glu Leu Arg Glu	Asp Asp Phe Gln Pro	Leu
380	385	390	
Met Gln Leu Pro	Asn Leu Ser Thr Ile	Asn Leu Gly Ile Asn	Phe
395	400	405	
Ile Lys Gln Ile	Asp Phe Lys Leu Phe	Gln Asn Phe Ser Asn	Leu
410	415	420	
Glu Ile Ile Tyr	Leu Ser Glu Asn Arg	Ile Ser Pro Leu Val	Lys
425	430	435	
Asp Thr Arg Gln	Ser Tyr Ala Asn Ser	Ser Ser Phe Gln Arg	His
440	445	450	
Ile Arg Lys Arg	Arg Ser Thr Asp Phe	Glu Phe Asp Pro His	Ser
455	460	465	
Asn Phe Tyr His	Phe Thr Arg Pro Leu	Ile Lys Pro Gln Cys	Ala
470	475	480	
Ala Tyr Gly Lys	Ala Leu Asp Leu Ser	Leu Asn Ser Ile Phe	Phe
485	490	495	
Ile Gly Pro Asn	Gln Phe Glu Asn Leu	Pro Asp Ile Ala Cys	Leu
500	505	510	
Asn Leu Ser Ala	Asn Ser Asn Ala Gln	Val Leu Ser Gly Thr	Glu
515	520	525	
Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr Asn	Asn
530	535	540	
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser	Asp
545	550	555	
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg	Ile
560	565	570	
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr	Asn
575	580	585	
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu	Thr
590	595	600	
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val	Phe
605	610	615	
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn	Arg
620	625	630	
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu	Asp

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Leu	Ser	Leu	Asn	Arg	Leu	Lys	His	Ile	Pro	Asn	Glu	Ala	Phe	Leu
				650					655					660
Asn	Leu	Pro	Ala	Ser	Leu	Thr	Glu	Leu	His	Ile	Asn	Asp	Asn	Met
				665					670					675
Leu	Lys	Phe	Phe	Asn	Trp	Thr	Leu	Leu	Gln	Gln	Phe	Pro	Arg	Leu
				680					685					690
Glu	Leu	Leu	Asp	Leu	Arg	Gly	Asn	Lys	Leu	Leu	Phe	Leu	Thr	Asp
				695					700					705
Ser	Leu	Ser	Asp	Phe	Thr	Ser	Ser	Leu	Arg	Thr	Leu	Leu	Leu	Ser
				710					715					720
His	Asn	Arg	Ile	Ser	His	Leu	Pro	Ser	Gly	Phe	Leu	Ser	Glu	Val
				725					730					735
Ser	Ser	Leu	Lys	His	Leu	Asp	Leu	Ser	Ser	Asn	Leu	Leu	Lys	Thr
				740					745					750
Ile	Asn	Lys	Ser	Ala	Leu	Glu	Thr	Lys	Thr	Thr	Thr	Lys	Leu	Ser
				755					760					765
Met	Leu	Glu	Leu	His	Gly	Asn	Pro	Phe	Glu	Cys	Thr	Cys	Asp	Ile
				770					775					780
Gly	Asp	Phe	Arg	Arg	Trp	Met	Asp	Glu	His	Leu	Asn	Val	Lys	Ile
				785					790					795
Pro	Arg	Leu	Val	Asp	Val	Ile	Cys	Ala	Ser	Pro	Gly	Asp	Gln	Arg
				800					805					810
Gly	Lys	Ser	Ile	Val	Ser	Leu	Glu	Leu	Thr	Thr	Cys	Val	Ser	Asp
				815					820					825
Val	Thr	Ala	Val	Ile	Leu	Phe	Phe	Phe	Thr	Phe	Phe	Ile	Thr	Thr
				830					835					840
Met	Val	Met	Leu	Ala	Ala	Leu	Ala	His	His	Leu	Phe	Tyr	Trp	Asp
				845					850					855
Val	Trp	Phe	Ile	Tyr	Asn	Val	Cys	Leu	Ala	Lys	Val	Lys	Gly	Tyr
				860					865					870
Arg	Ser	Leu	Ser	Thr	Ser	Gln	Thr	Phe	Tyr	Asp	Ala	Tyr	Ile	Ser
				875					880					885
Tyr	Asp	Thr	Lys	Asp	Ala	Ser	Val	Thr	Asp	Trp	Val	Ile	Asn	Glu
				890					895					900
Leu	Arg	Tyr	His	Leu	Glu	Glu	Ser	Arg	Asp	Lys	Asn	Val	Leu	Leu
				905					910					915
Cys	Leu	Glu	Glu	Arg	Asp	Trp	Asp	Pro	Gly	Leu	Ala	Ile	Ile	Asp
				920					925					930

Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val
 935 940 945
 Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe
 950 955 960
 Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile
 965 970 975
 Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu
 980 985 990
 Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro
 995 1000 1005
 Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 499

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<210> 500

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 500

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<210> 501

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

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<210> 504
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

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<210> 505
<211> 1738
<212> DNA
<213> Homo sapiens

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<211> 273
<212> PRT
<213> Homo sapiens

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Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
35 40 45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln
140 145 150

Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu
155 160 165

Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly
170 175 180

Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala
185 190 195

Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu
200 205 210

Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala
215 220 225

Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
230 235 240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
260 265 270

Lys Asp Ser

<210> 507
<211> 1700
<212> DNA
<213> Homo sapiens

Variable	Mean	SD	Min	Max
Age	34.5	10.2	18	65
Gender	0.52	0.50	0	1
Marital status	0.68	0.48	0	1
Education	12.5	1.5	9	16
Income	15.2	3.5	10	25
Health status	1.2	0.8	0	2
Stress level	2.5	1.2	1	4
Life satisfaction	3.8	1.0	2	5
Work engagement	4.2	0.8	3	5
Organizational commitment	4.5	0.7	3	5
Job satisfaction	4.1	0.9	3	5
Turnover intention	1.5	0.6	0	2
Organizational citizenship behavior	3.5	0.8	2	4
Employee well-being	3.2	0.9	2	4
Work-life balance	3.0	0.7	2	4
Perceived organizational support	3.8	0.8	2	4
Psychological safety	3.6	0.7	2	4
Trust in management	3.4	0.6	2	4
Employee voice	3.3	0.7	2	4
Employee engagement	3.1	0.6	2	4
Employee retention	2.9	0.5	2	4
Employee productivity	2.7	0.4	2	4
Employee turnover	2.5	0.3	2	4
Employee absenteeism	2.3	0.2	2	4
Employee commitment	2.1	0.2	2	4
Employee loyalty	1.9	0.1	2	4
Employee satisfaction	1.7	0.1	2	4
Employee well-being	1.5	0.1	2	4
Employee engagement	1.3	0.1	2	4
Employee retention	1.1	0.1	2	4
Employee productivity	0.9	0.1	2	4
Employee turnover	0.7	0.1	2	4
Employee absenteeism	0.5	0.1	2	4
Employee commitment	0.3	0.1	2	4
Employee loyalty	0.1	0.1	2	4
Employee satisfaction	0.0	0.1	2	4
Employee well-being	0.0	0.1	2	4
Employee engagement	0.0	0.1	2	4
Employee retention	0.0	0.1	2	4
Employee productivity	0.0	0.1	2	4
Employee turnover	0.0	0.1	2	4
Employee absenteeism	0.0	0.1	2	4
Employee commitment	0.0	0.1	2	4
Employee loyalty	0.0	0.1	2	4
Employee satisfaction	0.0	0.1	2	4
Employee well-being	0.0	0.1	2	4
Employee engagement	0.0	0.1	2	4
Employee retention	0.0	0.1	2	4
Employee productivity	0.0	0.1	2	4
Employee turnover	0.0	0.1	2	4
Employee absenteeism	0.0	0.1	2	4
Employee commitment	0.0	0.1	2	4
Employee loyalty	0.0	0.1	2	4
Employee satisfaction	0.0	0.1	2	4
Employee well-being	0.0	0.1	2	4
Employee engagement	0.0	0.1	2	4
Employee retention	0.0	0.1	2	4
Employee productivity	0.0	0.1	2	4
Employee turnover	0.0	0.1	2	4
Employee absenteeism	0.0	0.1	2	4
Employee commitment	0.0	0.1	2	4
Employee loyalty	0.0	0.1	2	4
Employee satisfaction	0.0	0.1	2	4
Employee well-being	0.0	0.1	2	4
Employee engagement	0.0	0.1	2	4
Employee retention	0.0	0.1	2	4
Employee productivity	0.0	0.1	2	4
Employee turnover	0.0	0.1	2	4
Employee absenteeism	0.0	0.1	2	4
Employee commitment	0.0	0.1	2	4
Employee loyalty	0.0	0.1	2	4
Employee satisfaction	0.0	0.1	2	4
Employee well-being	0.0	0.1	2	4
Employee engagement	0.0	0.1	2	4
Employee retention	0.0	0.1	2	4
Employee productivity	0.0	0.1	2	4
Employee turnover	0.0	0.1	2	4
Employee absenteeism	0.0	0.1	2	4
Employee commitment	0.0	0.1	2	4
Employee loyalty	0.0	0.1	2	4
Employee satisfaction	0.0	0.1	2	4
Employee well-being	0.0	0.1	2	4
Employee engagement	0.0	0.1	2	4
Employee retention	0.0	0.1	2	4
Employee productivity	0.0	0.1	2	4
Employee turnover</				

368

cccttctctcg ggaggctccc cagaccctgg catgggatgg gctgggatct 1500
 tctctgtgaa tocacccctg gctaccccca ccctggctac cccaacggca 1550
 tcccaaggcc aggtggaccc tcagctgagg gaaggtacga gctccctgct 1600
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 cctcagtggg ggctgctgcc tgacccccag cacaataaaa atgaaacgtg 1700

<210> 508
 <211> 273
 <212> PRT
 <213> Homo sapiens

<400> 508

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu	1	5	10	15
Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val	20	25	30	
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	35	40	45	
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	140	145	150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	155	160	165	
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	170	175	180	
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	185	190	195	
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	200	205	210	

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
			215						220					225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
			230						235					240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu
			245						250					255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys
			260						265					270
Lys	Asp	Ser												

<210> 509
 <211> 1538
 <212> DNA
 <213> Homo sapiens

<400> 509
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 ctgaggcccc agcaagggct agggctccatc tccagtccca ggacacagca 150
 gcggccacca tggccacgcc tgggctccag cagcatcagc agccccagg 200
 accggggagg cacaggtggc cccaccacc cggaggagca gctcctgccc 250
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 gccaccccgct ctggaggcac aggccatgag gggctctcag gaggtgctgc 350
 tgatgtggct tctggtgttg gcagtgggcg gcacagagca cgcctaccgg 400
 cccggccgta ggggtgtgtg tgtccgggct cacggggacc ctgtctccga 450
 gtcgttcgtg cagcgtgtgt accagccctt cctcaccacc tgcgacgggc 500
 accgggcctg cagcacctac cgaaccatct ataggaccgc ctaccgccgc 550
 agccctgggc tggccctgc caggcctcgc tacgctgct gcccgggctg 600
 gaagaggacc agcgggcttc ctggggcctg tggagcagca atatgccagc 650
 cgccatgccg gaacggaggg agctgtgtcc agcctggccg ctgcccgtgc 700
 cctgcaggat ggcggggtga cacttgccag tcagatgtgg atgaatgcag 750
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 actggtgcca gtgttgggag gggcacagcc tgtctgcaga cggtaactc 850
 tgtgtgcca agggaggggc cccaggggtg gcccacaacc cgacaggagt 900
 ggacagtgca atgaaggaag aagtgcagag gctgcagtcc agggtggaac 950

tgctggagga gaagctgcag ctggtgctgg cccactgca cagcctggcc 1000
 tcgcaggcac tggagcatgg gctcccggac cccggcagcc tcctggtgca 1050
 ctccctccag cagctcggcc gcacgactc cctgagcgag cagatttcct 1100
 tcctggagga gcagctgggg tcctgctcct gcaagaaaga ctctgtgactg 1150
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 tgcccctgcc caacatgctg ggggtccaga agccacctcg gggtgactga 1250
 gcggaaggcc aggcagggcc ttcctcctct tcctcctccc ctctcctggg 1300
 aggctcccca gaccctggca tgggatgggc tgggatcttc tctgtgaatc 1350
 caccctggc taccaccacc ctggctaccc caacggcatc ccaaggccag 1400
 gtgggcccctc agctgagga aggtacgagc tccctgctgg agcctgggac 1450
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 ctgctgctg acccccagca caataaaaat gaaacgtg 1538

<210> 510
 <211> 273
 <212> PRT
 <213> Homo sapiens

<400> 510
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 20 25 30
 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
 35 40 45
 Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
 50 55 60
 Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
 65 70 75
 Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
 80 85 90
 Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
 95 100 105
 Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
 110 115 120
 Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
 125 130 135
 Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln

	140		145		150
Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu					
	155		160		165
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly					
	170		175		180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala					
	185		190		195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu					
	200		205		210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala					
	215		220		225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu					
	230		235		240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu					
	245		250		255
Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys					
	260		265		270
Lys Asp Ser					

<210> 511
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 511
 tggagcagca atatgccagc c 21

<210> 512
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 512
 ttttcactc ctgtcgggtt gg 22

<210> 513
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 513
ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514
<211> 2690
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2039-2065
<223> unknown base

<400> 514
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ggagacagcc tcccggcccc gggaggacaa gtcgctgcca cctttggctg 100
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agttgggtct ccgtgtttca ggccggctcc cccttcctgg tctcccttct 200
cccgtgggc cggtttatcg ggaggagatt gtcttccagg gctagcaatt 250
ggacttttga tgatgtttga ccagcggca ggaatagcag gcaacgtgat 300
ttcaaagctg ggctcagcct ctgtttcttc tctcgtgtaa tcgcaaaacc 350
cattttggag caggaattcc aatcatgtct gtgatggtgg tgagaaagaa 400
ggtgacacgg aaatgggaga aactcccagg caggaacacc ttttgctgtg 450
atggccgct catgatggc cgcaaaaagg gcattttcta cctgaccctt 500
ttcctcatcc tggggacatg tacactcttc ttgcctttg agtgccgcta 550
cctggctgtt cagctgtctc ctgccatccc tgtatttgot gccatgtctt 600
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tcaagaattt ccagataaac aaccagattg tgaaactgaa atactgttac 800
acatgcaaga tcttccggcc tcccggggcc tccattgca gcattctgtga 850
caactgtgtg gagcgcttcg accatcactg cccctgggtg gggaattgtg 900
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actggatttc atactttcct cgtggctctc aaccagacaa ccaatgaaga 1150
catcaaagga tcatggacag ggaagaatcg cgtccagaat ccctacagcc 1200
atggcaatat tgtgaagaac tgctgtgaag tgctgtgtgg ccccttgccc 1250
cccagtgtgc tggatcgaag gggatatttg ccactggagg aaagtggaag 1300
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ccttttagga atgggacagg taccttccac ttgttgtann nnnnnnnnn 2050
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caggaatggc agtaataaaa gtctgcactt tggtcatttc ttttcctcag 2150
aggaagcccg agtgctcact taaacactat cccctcagac tccctgtgtg 2200
aggcctgcag aggccctgaa tgcacaaatg ggaaaccaag gcacagagag 2250
gctctcctct cctctcctct ccccgatgt accctcaaaa aaaaaaaaaat 2300
gctaaccagt tcttccatta agcctcggt gagtgaggga aagcccagca 2350
ctgctgcct ctcggtaac tcaccctaag gcctcgccc acctctggt 2400
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caccggcaga gtcccagagc cacttcaccc tgggggtggg ctgtggcccc 2500
cagtcagctc tgctcaggac ctgctctatt tcagggaaga agatttatgt 2550

attatatgtg gctatatattc ctagagcacc tgtgttttcc tctttctaag 2600
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ttttcatcta tttgaaggcg attaaactgt gtctaatagca 2690

<210> 515
<211> 364
<212> PRT
<213> Homo sapiens

<400> 515
Met Ser Val Met Val Val Arg Lys Lys Val Thr Arg Lys Trp Glu
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Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met
20 25 30
Met Ala Arg Gln Lys Gly Ile Phe Tyr Leu Thr Leu Phe Leu Ile
35 40 45
Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu
50 55 60
Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu
65 70 75
Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp
80 85 90
Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile
95 100 105
Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln
110 115 120
Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile
125 130 135
Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro
140 145 150
Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe
155 160 165
Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn
170 175 180
Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr
185 190 195
Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser
200 205 210
Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr
215 220 225
Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val

230	235	240
Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr	245	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val	260	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu	275	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly	290	300
Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln	305	315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu	320	330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu	335	345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala	350	360
Glu Ala Glu Lys		

<210> 516
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 38, 88, 118, 135, 193, 213, 222
 <223> unknown base

<400> 516
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 tgaattaggt attataggga tgggtggggtt gatttttntt cctggaggct 100
 tttggctttg gactctcnct ttctcccaca gagcncttcg accatcactg 150
 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200
 tcttcacctt ttntctctcc cncctcaca totatgtcctt ogccttcaac 250
 atcgt 255

<210> 517
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 517

caacgtgatt tcaaagctgg gctc 24

<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtgaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

ctcacctgaa atctctcata gcc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

cgcaaaaccc attttgggag caggaattcc aatcatgtct gtgatggtgg 50

<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

gttgtgtcct tcagcaaaac agtggattta aatctccttg cacaagcttg 50

agagcaacac aatctatcag gaaagaaaga aagaaaaaaa ccgaacctga 100

caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150
aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200
tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc caccttcccc 250
aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300
gtgcactatt gacaaccggg tccccgggt gccctggcta aaccgcagca 350
ccatcctcta tgctgggaat gacaagtggg gcctggatcc tcgctggtc 400
cttctgagca acacccaaac gcagtacagc atcgagatcc agaactgga 450
tgtgtatgac gagggccctt acacctgctc ggtgcagaca gacaaccacc 500
caaagacctc taggggtccac ctcatgtgc aagtatctcc caaaattgta 550
gagatttctt cagatatctc cattaatgaa gggaacaata ttagcctcac 600
ctgcatagca actggtagac cagagcctac ggttacttgg agacacatct 650
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catacatttc agaagccaag ggtacaggtg tccccgtggg aaaaaagggg 850
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caaggatgac aaaagactga ttgaaggaaa gaaaggggtg aaagtggaaa 950
acagaccttt cctctcaaaa ctcatcttct tcaatgtctc tgaacatgac 1000
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cagcatcatg ctatttggtc caggcgccgt cagcgaggtg agcaacggca 1100
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gccgccacca ccaccacca cacaacagca atggcaacac cgacagcaac 1250
caatcagata tatacaaatg aaattagaag aaacacagcc tcatgggaca 1300
gaaatttgag ggaggggaac aaagaatact ttggggggaa aagagtttta 1350
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tctgcccaca gagtgcccc acgtggaaca ttctggagct ggccatcca 1550

aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600
 gtggcgctgc gggcactttg gtagactgtg ccaccacggc gtgtgttgtg 1650
 aaacgtgaaa taaaaagagc aaaaaaaaaa 1679

<210> 523
 <211> 344
 <212> PRT
 <213> Homo sapiens

<400> 523

Met	Lys	Thr	Ile	Gln	Pro	Lys	Met	His	Asn	Ser	Ile	Ser	Trp	Ala	
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Ile	Phe	Thr	Gly	Leu	Ala	Ala	Leu	Cys	Leu	Phe	Gln	Gly	Val	Pro	
				20					25					30	
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val	
				35					40					45	
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp	
				50					55					60	
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu	
				65					70					75	
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu	
				80					85					90	
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val	
				95					100					105	
Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp	
				110					115					120	
Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser	
				125					130					135	
Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly	
				140					145					150	
Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro	
				155					160					165	
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val	
				170					175					180	
Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln	
				185					190					195	
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro	
				200					205					210	
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile	
				215					220					225	
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr	

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230	235	240
Leu Gln Cys Glu Ala Ser Ala Val Pro	Ser Ala Glu Phe Gln Trp	
245	250	255
Tyr Lys Asp Asp Lys Arg Leu Ile Glu	Gly Lys Lys Gly Val Lys	
260	265	270
Val Glu Asn Arg Pro Phe Leu Ser Lys	Leu Ile Phe Phe Asn Val	
275	280	285
Ser Glu His Asp Tyr Gly Asn Tyr Thr	Cys Val Ala Ser Asn Lys	
290	295	300
Leu Gly His Thr Asn Ala Ser Ile Met	Leu Phe Gly Pro Gly Ala	
305	310	315
Val Ser Glu Val Ser Asn Gly Thr Ser	Arg Arg Ala Gly Cys Val	
320	325	330
Trp Leu Leu Pro Leu Leu Val Leu His	Leu Leu Leu Lys Phe	
335	340	

<210> 524
 <211> 503
 <212> DNA
 <213> Homo sapiens

<400> 524
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 Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu
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 Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile
 65 70 75
 Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser
 80 85 90
 Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn
 95 100 105
 Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr
 110 115 120
 Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln Val
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 Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu
 140 145 150
 Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu
 155 160 165
 Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe
 170 175 180
 Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln
 185 190 195
 Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro
 200 205 210
 Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile
 215 220 225
 Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu

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Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	
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Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	
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 aactcacctg ggtccgctg agccatgagc acttgctgca gcgggtagac 500
 aacttcactc agaaccagg gatgttcaga atcaaagggtg aacaaggcgc 550
 cccaggtctt caaggtcaca agggggccat gggcatgcct ggtgcccctg 600
 gcccgcgggg accacctgct gagaaggag ccaagggggc tatgggacga 650

gatggagcaa caggccccctc gggaccccaa ggcccaccgg gagtcaaggg 700
agagggcgggc ctccaaggac cccaggggtgc tccaggggaag caaggagcca 750
ctggcacccc aggaccccaa ggagagaagg gcagcaaagg cgatgggggt 800
ctcattggcc caaaagggga aactggaact aaggagaga aaggagacct 850
gggtctccca ggaagcaaag gggacagggg catgaaagga gatgcagggg 900
tcattggggcc tcctggagcc caggggagta aaggtgactt cgggaggcca 950
ggcccaccag gtttggtctg ttttcctgga gctaaaggag atcaaggaca 1000
acctggactg caggggtgtt cgggccctcc tggcgagtg ggacaccag 1050
gtgccaaggg tgagcctggc agtgctggct cccctgggcg agcaggactt 1100
ccagggagcc cggggagtc aggagccaca ggcctgaaag gaagcaaagg 1150
ggacacagga cttcaaggac agcaaggaag aaaaggagaa tcaggagtgc 1200
caggccctgc aggtgtgaag ggagaacagg ggagcccagg gctggcaggt 1250
cccaagggag cccctggaca agctggccag aaggagagacc agggagtga 1300
aggatcttct ggggagcaag gagtaaagg agaaaaagg gaaagaggtg 1350
aaaactcagt gtccgtcagg attgtcggca gtagtaacc aggccgggct 1400
gaagtttact acagtgggtac ctgggggaca atttgcgat acgagtggca 1450
aaattctgat gccattgtct tctgccgat gctgggttac tccaaaggaa 1500
gggccctgta caaagtggga gctggcactg ggagatctg gctggataat 1550
gttcagtgtc ggggcacgga gattaccctg tggagctgca ccaagaatag 1600
ctggggccat catgactgca gccacgagga ggacgcaggc gtggagtga 1650
gcgtctgacc cggaaccct ttcacttctc tgctcccgag gtgtcctcgg 1700
gctcatatgt ggaaggcag aggatctctg aggagttccc tggggacaac 1750
tgagcagcct ctggagaggg gccattaata aagctcaaca tcattga 1797

<210> 614
<211> 520
<212> PRT
<213> Homo Sapien

<400> 614
Met Arg Asn Lys Lys Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu
1 5 10 15
Thr Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu
20 25 30

Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	
				35					40					45	
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	
				50					55					60	
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	
				65					70					75	
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	
				80					85					90	
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	
				95					100					105	
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	
				110					115					120	
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	
				125					130					135	
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	
				140					145					150	
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	
				155					160					165	
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	
				170					175					180	
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln	
				185					190					195	
Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln	
				200					205					210	
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln	
				215					220					225	
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys	
				230					235					240	
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro	
				245					250					255	
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met	
				260					265					270	
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro	
				275					280					285	
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln	
				290					295					300	
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val	
				305					310					315	
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro	

320	325	330
Gly Arg Ala Gly Leu Pro Gly Ser Pro	Gly Ser Pro Gly Ala Thr	
335	340	345
Gly Leu Lys Gly Ser Lys Gly Asp Thr	Gly Leu Gln Gly Gln Gln	
350	355	360
Gly Arg Lys Gly Glu Ser Gly Val Pro	Gly Pro Ala Gly Val Lys	
365	370	375
Gly Glu Gln Gly Ser Pro Gly Leu Ala	Gly Pro Lys Gly Ala Pro	
380	385	390
Gly Gln Ala Gly Gln Lys Gly Asp Gln	Gly Val Lys Gly Ser Ser	
395	400	405
Gly Glu Gln Gly Val Lys Gly Glu Lys	Gly Glu Arg Gly Glu Asn	
410	415	420
Ser Val Ser Val Arg Ile Val Gly Ser	Ser Asn Arg Gly Arg Ala	
425	430	435
Glu Val Tyr Tyr Ser Gly Thr Trp Gly	Thr Ile Cys Asp Asp Glu	
440	445	450
Trp Gln Asn Ser Asp Ala Ile Val Phe	Cys Arg Met Leu Gly Tyr	
455	460	465
Ser Lys Gly Arg Ala Leu Tyr Lys Val	Gly Ala Gly Thr Gly Gln	
470	475	480
Ile Trp Leu Asp Asn Val Gln Cys Arg	Gly Thr Glu Ser Thr Leu	
485	490	495
Trp Ser Cys Thr Lys Asn Ser Trp Gly	His His Asp Cys Ser His	
500	505	510
Glu Glu Asp Ala Gly Val Glu Cys Ser	Val	
515	520	

<210> 615
 <211> 647
 <212> DNA
 <213> Homo Sapien

<400> 615
 cccacgcgtc cgaaggcaga caaagggttca ttgtgtaaaga agctccttcc 50
 agcacctcct ctctttctcct ttgcccacaa ctcaccaggt gagtgtgagc 100
 atttaagaag catcctctgc caagaccacaa aggaaagaag aaaaagggcc 150
 aaaagccaaa atgaaactga tggtaacttgt ttccaccatt gggctaactt 200
 tgctgctagg agttcaagcc atgcctgcaa atgcctcttc ttgctacaga 250
 aagatactaa aagatcacaa ctgtcacacac cttccggaag gagtagctga 300

cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350
 gatgtgagat gatctgttac tgcaacttca gcgaattgct ctgctgcca 400
 aaagacgttt tctttggacc aaagatctct ttcgtgattc cttgcaacaa 450
 tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttcccac 500
 aaactgcact acatcagtat aactgcattt ctagtttcta tatagtcaa 550
 tagagcatag attctataaa ttcttacttg tctaagacaa gtaaattctgt 600
 gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaaa 647

<210> 616
 <211> 98
 <212> PRT
 <213> Homo Sapien

<400> 616
 Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu
 1 5 10 15
 Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg
 20 25 30
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
 35 40 45
 Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp
 50 55 60
 Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu
 65 70 75
 Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser
 80 85 90
 Phe Val Ile Pro Cys Asn Asn Gln
 95

<210> 617
 <211> 2558
 <212> DNA
 <213> Homo Sapien

<400> 617
 cccacgcgtc cgcggacgcg tgggctggac cccaggtctg gagcgaattc 50
 cagcctgcag ggctgataag cgaggcatta gtgagattga gagagacttt 100
 accccgccgt ggtggttggg gggcgcgag tagagcagca gcacaggcgc 150
 gggccccggg aggcggctc tgctcgcgcc gagatgtgga atctccttca 200
 cgaaaccgac tcggctgtgg ccaccgcgcg ccgcccgcgc tggctgtgcg 250
 ctggggcgct ggtgctggcg ggtggcttct ttctcctcgg cttcctcttc 300

ggggtggttta taaaatcctc caatgaagct actaacatta ctccaaagca 350
 taatatgaaa gcatttttgg atgaattgaa agctgagaac atcaagaagt 400
 tottacataa ttttacacag ataccacatt tagcaggaac agaacaaaac 450
 tttcagcttg caaagcaa atcaatcccag tggaaagaat ttggcctgga 500
 ttctgttgag ctagctcatt atgatgtcct gttgtcctac ccaaataaga 550
 ctcatcccaa ctacatctca ataattaatg aagatggaaa tgagattttc 600
 aacacatcat tatttgaacc acctcctcca ggatatgaaa atgtttcgga 650
 tattgtacca cttttcagtg ctttctctcc tcaaggaatg ccagagggcg 700
 atctagtgtg tgtaaactat gcacgaactg aagacttctt taaattggaa 750
 cgggacatga aaatcaattg ctctgggaaa attgtaattg ccagatatgg 800
 gaaagttttc agaggaaata aggttaaaaa tgcccagctg gcagggggcca 850
 aaggagtcac tctctactcc gacctgctg actactttgc tcctgggggtg 900
 aagtcctatc cagacggttg gaatcttctt ggaggtgggtg tccagcgtgg 950
 aaatatccta aatctgaatg gtgcaggaga ccctctcaca ccaggttacc 1000
 cagcaaatga atatgcttat aggcgtggaa ttgcagaggc tgttgggtctt 1050
 ccaagtattc ctgttcatcc aattggatac tatgatgcac agaagctcct 1100
 agaaaaaatg ggtggctcag caccaccaga tagcagctgg agaggaagtc 1150
 tcaaagtgcc ctacaatgtt ggacctgggt ttactggaaa cttttctaca 1200
 caaaaagtca agatgcacat ccactotacc aatgaagtga cgagaattta 1250
 caatgtgata ggtactctca gaggagcagt ggaaccagac agatatgtca 1300
 ttctgggagg tcaccgggac tcatgggtgt ttggtggtat tgaccctcag 1350
 agtggagcag ctgttggtca tgaaattgtg aggagctttg gaacactgaa 1400
 aaaggaaggg tggagacctg gaagaacaat tttgtttgca agctgggatg 1450
 cagaagaatt tgggtcttctt ggttctactg agtgggcaga ggagaattca 1500
 agactccttc aagagcgtgg cgtggcttat attaattgctg actcatctat 1550
 agaaggaaac tacactctga gagttgattg tacaccgctg atgtacagct 1600
 tggtagacaa cctaacaaaa gagctgaaaa gccctgatga aggctttgaa 1650
 ggcaaatctc tttatgaaag ttggactaaa aaaagtcctt cccagagtt 1700
 cagtggcatg cccaggataa gcaaattggg atctggaaat gattttgagg 1750

tgttcttcca acgacttga attgcttcag gcagagcacg gtatactaaa 1800
 aattgggaaa caaacaatt cagcggctat ccactgtatc acagtgtcta 1850
 tgaaacatat gagttggtgg aaaagtttta tgatccaatg tttaaatata 1900
 acctcactgt ggcccagggt cgaggaggga tgggtgttga gctagccaat 1950
 tccatagtgc tcccttttga ttgtcgagat tatgctgtag ttttaagaaa 2000
 gtatgctgac aaaatctaca gtatttctat gaaacatcca caggaaatga 2050
 agacatacag tgtatcattt gattcacttt tttctgcagt aaagaatttt 2100
 acagaaattg cttccaagtt cagtgcagaga ctccaggact ttgacaaaag 2150
 caaccaata gtattaagaa tgatgaatga tcaactcatg tttctggaaa 2200
 gagcatttat tgatocatta gggttaccag acaggccttt ttataggcat 2250
 gtcacttatg ctccaagcag ccacaacaag tatgcagggg agtcattccc 2300
 aggaatttat gatgctctgt ttgatattga aagcaaagtg gacccttcca 2350
 aggcctgggg agaagtgaag agacagattt atgttgcagc cttcacagt 2400
 caggcagctg cagagacttt gagtgaagta gcctaagagg attttttaga 2450
 gaatccgtat tgaatttgtg tggatatgtca ctacagaaaga atcgtaatgg 2500
 gtatatatgat aaatttttaa attgggtatat ttgaaataaa gttgaatatt 2550
 atatataa 2558

<210> 618
 <211> 750
 <212> PRT
 <213> Homo Sapien

<400> 618
 Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala
 1 5 10 15
 Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly
 20 25 30
 Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser
 35 40 45
 Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
 50 55 60
 Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His
 65 70 75
 Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe
 80 85 90

Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	95	100	105
Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	110	115	120
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	125	130	135
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly	140	145	150
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser	155	160	165
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	170	175	180
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn	185	190	195
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	200	205	210
Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val	215	220	225
Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys	230	235	240
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	245	250	255
Gly	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	260	265	270
Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	275	280	285
Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	290	295	300
Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	305	310	315
Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	320	325	330
Pro	Gly	Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	335	340	345
Ile	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	350	355	360
Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	365	370	375
Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser			

	380		385		390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr	Leu		
	395	400	405		
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala	Ser		
	410	415	420		
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp	Ala		
	425	430	435		
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr	Ile		
	440	445	450		
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val	Asp		
	455	460	465		
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys	Glu		
	470	475	480		
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr	Glu		
	485	490	495		
Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro		
	500	505	510		
Arg Ile Ser Lys	Leu Gly Ser Gly Asn	Asp Phe Glu Val Phe	Phe		
	515	520	525		
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys	Asn		
	530	535	540		
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser	Val		
	545	550	555		
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met	Phe		
	560	565	570		
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val	Phe		
	575	580	585		
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp	Tyr		
	590	595	600		
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile	Ser		
	605	610	615		
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Phe	Asp		
	620	625	630		
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser	Lys		
	635	640	645		
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile	Val		
	650	655	660		
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala	Phe		
	665	670	675		

Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	His	Val
				680					685					690
Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	Phe
				695					700					705
Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp
				710					715					720
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala
				725					730					735
Ala	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Ser	Glu	Val	Ala
				740					745					750

<210> 619

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 619

agatgtgaag gtgcaggtgt gccg 24

<210> 620

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 620

gaacatcagc gctcccggtta attcc 25

<210> 621

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 621

ccagcctttg aatggtacaa aggagagaag aagctcttca atggcc 46

<210> 622

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 622

ccaaactcac ccagtgagtg tgagc 25

<210> 623
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 623
tgggaaatca ggaatggtgt tctcc 25

<210> 624
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide probe

<400> 624
cttgttttca ccattgggct aactttgctg ctaggagttc aagccatgcc 50

10340464650